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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:57:26 ; Search time 18 Seconds  
(without alignments)  
184.984 Million cell updates/sec

Title: US-09-540-843-11  
Perfect score: 6  
Sequence: 1 ttaggg 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0  
Maximum DB seq length: 200

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	6	1	US-08-381-097A-3
2	6	100.0	6	1	US-08-381-097A-5
3	6	100.0	6	1	US-08-153-051B-4
4	6	100.0	6	1	US-08-337-684-2
5	6	100.0	6	2	US-08-151-477A-4
6	6	100.0	6	2	US-08-670-999-3
7	6	100.0	6	3	US-08-729-598-4
8	6	100.0	6	3	US-08-819-867-9
9	6	100.0	6	3	US-08-819-867-27
10	6	100.0	6	3	US-08-630-019A-1
11	6	100.0	6	3	US-09-018-545-3
12	6	100.0	6	3	US-09-114-399-3
13	6	100.0	6	4	US-09-608-636A-1
14	6	100.0	6	4	US-09-378-535-9
15	6	100.0	6	4	US-09-378-535-27
16	6	100.0	6	4	US-09-940-173A-1
17	6	100.0	6	5	PCT-US96-01206-1
18	6	100.0	7	3	US-08-729-598-8
19	6	100.0	7	4	US-09-940-173A-6
20	6	100.0	8	3	US-08-838-545-15
21	6	100.0	8	3	US-08-838-545-30
22	6	100.0	8	3	US-08-838-545-34
23	6	100.0	8	3	US-09-349-532-15
24	6	100.0	8	3	US-09-349-532-30
25	6	100.0	8	3	US-09-349-532-34
26	6	100.0	8	4	US-09-940-173A-4
27	6	100.0	9	1	US-08-337-684-3

28	6	100.0	9	3	US-08-630-019A-27	Sequence 27, Appl
29	6	100.0	9	3	US-09-069-434-14	Sequence 14, Appl
30	6	100.0	9	3	US-08-838-545-16	Sequence 16, Appl
31	6	100.0	9	3	US-09-349-532-16	Sequence 16, Appl
32	6	100.0	10	1	US-08-192-300-18	Sequence 18, Appl
33	6	100.0	10	2	US-08-531-743-10	Sequence 10, Appl
34	6	100.0	10	3	US-08-630-019A-8	Sequence 8, Appl
35	6	100.0	10	3	US-08-838-545-7	Sequence 7, Appl
36	6	100.0	10	3	US-08-838-545-11	Sequence 11, Appl
37	6	100.0	10	3	US-08-838-545-17	Sequence 17, Appl
38	6	100.0	10	3	US-08-838-545-21	Sequence 21, Appl
39	6	100.0	10	3	US-08-838-545-29	Sequence 29, Appl
40	6	100.0	10	3	US-08-974-549A-527	Sequence 527, App
41	6	100.0	10	3	US-09-349-532-7	Sequence 7, Appl
42	6	100.0	10	3	US-09-349-532-11	Sequence 11, Appl
43	6	100.0	10	3	US-09-349-532-17	Sequence 17, Appl
44	6	100.0	10	3	US-09-349-532-21	Sequence 21, Appl
45	6	100.0	10	3	US-09-349-532-29	Sequence 29, Appl

## ALIGNMENTS

RESULT 1  
US-08-381-097A-3  
; Sequence 3, Application US/08381097A  
; Patent No. 5643890  
; GENERAL INFORMATION:  
; APPLICANT: Iverson, Patrick L.  
; TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides  
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment  
; TITLE OF INVENTION: of Cancer and Other Diseases  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Zarely, McKee, Thomte, Voorhees, & Sease  
; STREET: 801 Grand Suite 3200  
; CITY: Des Moines  
; STATE: Iowa  
; COUNTRY: United States  
; ZIP: 50309  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,097A  
; FILING DATE: 31-JAN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nebel, Heidi S  
; REGISTRATION NUMBER: 37,719  
; REFERENCE/DOCKET NUMBER: ummc 63092  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 515-288-3667  
; TELEFAX: 515-288-1338  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-381-097A-3

Query Match 100.0%; Score 6; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTAGGG 6

Db 1 TTAGG 6

RESULT 2

US-08-381-097A-5/c  
Sequence 5, Application US/08381097A  
Patent No. 5643890  
GENERAL INFORMATION:  
APPLICANT: Iverson, Patrick L.  
APPLICANT: Mata, John E.  
TITLE OF INVENTION: Synthetic Oligodeoxynucleotides  
TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment  
TITLE OF INVENTION: of Cancer and Other Diseases  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease  
STREET: 801 Grand Suite 3200  
CITY: Des Moines  
STATE: Iowa  
COUNTRY: United States  
ZIP: 50309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/381,097A  
FILING DATE: 31-JAN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Nebel, Heidi S  
REGISTRATION NUMBER: 37,719  
REFERENCE/DOCKET NUMBER: ummc 63092  
TELEPHONE: 515-288-3667  
TELEFAX: 515-288-1338  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-381-097A-5

Query Match 100.0%; Score 6; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGG 6  
Db 6 TTAGG 1

RESULT 3

US-08-153-051B-4/c  
Sequence 4, Application US/08153051B  
Patent No. 5645986  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,051B  
FILING DATE: No. 5645986ember 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 204/195  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-153-051B-4

Query Match 100.0%; Score 6; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGG 6  
Db 6 TTAGG 1

RESULT 4

US-08-337-684-2  
Sequence 2, Application US/08337684  
Patent No. 5686306  
GENERAL INFORMATION:  
APPLICANT: West, Michael David  
APPLICANT: Shay, Jerry  
APPLICANT: Wright, Woodring E.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR  
TITLE OF INVENTION: MEASURING TELOMERES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA: US/08/337,684  
APPLICATION NUMBER: 08/151,477A  
FILING DATE: No. 5686306ember 12, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/151,477  
FILING DATE: No. 5686306ember 12, 1993  
APPLICATION NUMBER: 08/153,051  
FILING DATE: No. 5686306ember 12, 1993  
APPLICATION NUMBER: 08/060,952  
FILING DATE: May 13, 1993  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/085  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-337-684-2

Query Match 100.0%; Score 6; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTAGGG 6  
Db 1 TTAGGG 6

RESULT 5  
US-08-151-477A-4/c  
Sequence 4, Application US/08151477A  
Patent No. 5830844  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: California  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,477A  
FILING DATE: No. 5830644ember 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-151-477A-4

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTAGGG 6  
Db 6 TTAGGG 1

RESULT 6  
US-08-670-999-3  
Sequence 3, Application US/08670999  
Patent No. 5849727  
GENERAL INFORMATION:  
APPLICANT: Porter, Thomas R.  
APPLICANT: Iverson, Patrick L.  
TITLE OF INVENTION: Compositions and Methods for Altering  
TITLE OF INVENTION: the Biodistribution of Biological Agents  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease  
STREET: 801 Grand Suite 3200  
CITY: Des Moines  
STATE: Iowa  
COUNTRY: United States  
ZIP: 50309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/670,999  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Nebel, Heidi S.  
REGISTRATION NUMBER: 37,719  
REFERENCE/DOCKET NUMBER: unmc 107A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 515-288-3667  
TELEFAX: 515-288-1338  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO

ANTI-SENSE: YES  
US-08-670-999-3

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

## RESULT 7

US-08-729-598-4  
Sequence 4, Application US/08729598  
Patent No. 6001657

GENERAL INFORMATION:

APPLICANT: Hardin, Charles C.

APPLICANT: Brown II, Bernard A.

APPLICANT: Roberts, John J.

APPLICANT: Pellsue, Stephen A.

TITLE OF INVENTION: Antibodies That Selectively Bind

TITLE OF INVENTION: Quadruplex Nucleic Acids

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sorojini J. Biswas

STREET: P.O. Box 37428

CITY: Raleigh

STATE: No. 6001657th Carolina

COUNTRY: USA

ZIP: 27627

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/729,598

FILING DATE: 11-OCT-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Biswas, Sorojini J.

REGISTRATION NUMBER: 39,111

REFERENCE/DOCKET NUMBER: 5051-301A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 854-1400

TELEFAX: (919) 854-1401

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: DNA (genomic)

US-08-729-598-4

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

## RESULT 8

US-08-819-867-9

Sequence 9, Application US/08819867

Patent No. 6007989

GENERAL INFORMATION:

APPLICANT: Michael D. West

APPLICANT: Calvin B. Harley

APPLICANT: Scott L. Weinrich

APPLICANT: Catherine M. Strahl  
APPLICANT: Michael J. Meeachern  
APPLICANT: Jerry Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth H. Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO  
TITLE OF INVENTION: TELOMERASE LENGTH AND/OR  
TITLE OF INVENTION: TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,867  
FILING DATE: March 14, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/153,051  
FILING DATE: No. 6007989ember 12, 1993  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-819-867-9

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

## RESULT 9

US-08-819-867-27/c

Sequence 27, Application US/08819867

Patent No. 6007989

GENERAL INFORMATION:

APPLICANT: Michael D. West

APPLICANT: Calvin B. Harley

APPLICANT: Scott L. Weinrich

APPLICANT: Catherine M. Strahl

APPLICANT: Michael J. Meeachern

APPLICANT: Jerry Shay

APPLICANT: Woodring E. Wright

APPLICANT: Elizabeth H. Blackburn

APPLICANT: Nam Woo Kim  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO  
TITLE OF INVENTION: TEOLOMERE LENGTH AND/OR  
TITLE OF INVENTION: TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,867  
FILING DATE: March 14, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/153,051  
FILING DATE: No. 600799 September 12, 1993  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-819-867-27

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
Db 6 TTAGGG 1

RESULT 10  
US-08-630-019A-1  
Sequence 1, Application US/08G30019A  
Patent No. 6015710  
GENERAL INFORMATION:  
APPLICANT: Shay, Jerry W.  
APPLICANT: Wright, Woodring E.  
APPLICANT: Piatyszek, Mieczyslaw A.  
APPLICANT: Corey, David  
APPLICANT: No. 6015710, James C.  
TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
TITLE OF INVENTION: Peptide Nucleic Acids  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,019A  
FILING DATE: 09-JUN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "peptide nucleic acid (PNA),  
DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by  
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via  
DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"

US-08-630-019A-1

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTAGGG 6  
Db 1 TTAGGG 6

RESULT 11  
US-09-018-545-3  
Sequence 3, Application US/09018545  
Patent No. 6087493  
GENERAL INFORMATION:  
APPLICANT: Wheelhouse, Richard T.  
APPLICANT: Hurley, Laurence H.  
TITLE OF INVENTION: PORPHYRIN COMPOUNDS AS TELOMERASE  
TITLE OF INVENTION: INHIBITORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/018,545  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/037,295  
FILING DATE: 05-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UT5B:654

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-018-545-3

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
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QY 1 TTAGGG 6  
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Db 1 TTAGGG 6

RESULT 12  
US-09-114-399-3  
Sequence 3, Application US/09114399  
Patent No. 6245747  
GENERAL INFORMATION:  
APPLICANT: Porter, Thomas R.  
APPLICANT: Iversen, Patrick L.  
APPLICANT: Meyer, Gary D.  
TITLE OF INVENTION: Targeted Site Specific Drug Delivery  
TITLE OF INVENTION: Compositions and Method of Use  
FILE REFERENCE: 0450-0310.31  
CURRENT APPLICATION NUMBER: US/09/114,399  
CURRENT FILING DATE: 1998-07-13  
PRIOR APPLICATION NUMBER: US 08/615,495  
PRIOR FILING DATE: 1996-03-12  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PS-ODN  
US-09-114-399-3

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Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
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Db 1 TTAGGG 6

RESULT 13  
US-09-608-636A-1  
Sequence 1, Application US/09608636A  
Patent No. 6518268  
GENERAL INFORMATION:  
APPLICANT: Geron Corporation  
APPLICANT: Kyowa Hakko Kogyo Co., Ltd.  
APPLICANT: Chin, Allison C.  
APPLICANT: Holcomb, Ryan C.  
APPLICANT: Piatyszek, Mieczyslaw A  
APPLICANT: Singh, Upinder  
APPLICANT: Tolman, Richard L.  
APPLICANT: Akama, Tsutomu  
APPLICANT: Kanda, Yutaka  
APPLICANT: Asai, Akira  
APPLICANT: Yamashita, Yoshinori  
APPLICANT: Endo, Kaori  
APPLICANT: Yamaguchi, Hiroyuki  
TITLE OF INVENTION: Telomerase Inhibitors and Methods of Their Use

FILE REFERENCE: 055/003  
CURRENT APPLICATION NUMBER: US/09/608,636A  
CURRENT FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/142,173  
PRIOR FILING DATE: 1999-07-10  
PRIOR APPLICATION NUMBER: JP 11-187616  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: JP 11-307576  
PRIOR FILING DATE: 1999-10-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide  
US-09-608-636A-1

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Best Local Similarity 100.0%; Pred. No. 8.7e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

RESULT 14  
US-09-378-535-9  
Sequence 9, Application US/09378535  
Patent No. 6551774  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
Calvin B. Harley  
Scott L. Weinrich  
Catherine M. Strahl  
Michael J. Meeachern  
Jerry Shay  
Woodring E. Wright  
Elizabeth H. Blackburn  
Nam Woo Kim  
Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,535  
FILING DATE: 20-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/819,867  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-378-535-9

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
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Db 1 TTAGGG 6

RESULT 15
US-09-378-535-27/c
; Sequence 27, Application US/09378535
; Patent No. 6551774
; GENERAL APPLICANT:
; APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. Mceachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,535
; FILING DATE: 20-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/819,867
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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US-09-378-535-27

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Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6
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Db 6 TTAGGG 1

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Job time : 18 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:38:14 ; Search time 380.903 Seconds  
(without alignments)  
682.741 Million cell updates/sec

Title: US-09-540-843-11  
Perfect score: 6  
Sequence: 1 ttaggg 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0  
Maximum DB seq length: 200

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

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8: gb\_pl:\*

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31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 2	6	100.0	6	6	AX058275	Sequence
C 3	6	100.0	6	6	AX175285	Sequence
C 4	6	100.0	6	6	AX268763	Sequence
C 5	6	100.0	6	6	AX268764	Sequence
C 6	6	100.0	8	6	BD230086	Method fo
C 7	6	100.0	8	6	BD071049	Modulatio
C 8	6	100.0	8	6	BD071063	Modulatio
C 9	6	100.0	8	6	BD071067	Modulatio
C 10	6	100.0	9	6	BD071050	Modulatio
C 11	6	100.0	10	6	AR026485	Sequence
C 12	6	100.0	10	6	BD238638	Preparati
C 13	6	100.0	10	6	BD238940	Preparati
C 14	6	100.0	10	6	BD239195	Preparati
C 15	6	100.0	10	6	BD240276	Preparati
C 16	6	100.0	10	6	E36980	Human telom
C 17	6	100.0	10	6	AR243501	Sequence
C 18	6	100.0	10	6	AR336866	Sequence
C 19	6	100.0	10	6	AR390657	Sequence
C 20	6	100.0	10	6	AR393271	Sequence
C 21	6	100.0	10	6	AX152177	Sequence
C 22	6	100.0	10	6	AX153381	Sequence
C 23	6	100.0	10	6	AX153382	Sequence
C 24	6	100.0	10	6	AX153383	Sequence
C 25	6	100.0	10	6	AX153524	Sequence
C 26	6	100.0	10	6	AX753493	Sequence
C 27	6	100.0	10	6	AX810562	Sequence
C 28	6	100.0	10	6	BD011231	Human tel
C 29	6	100.0	10	6	BD023724	Method fo
C 30	6	100.0	10	6	BD071041	Modulatio
C 31	6	100.0	10	6	BD071045	Modulatio
C 32	6	100.0	10	6	BD071051	Modulatio
C 33	6	100.0	10	6	BD071054	Modulatio
C 34	6	100.0	10	6	BD071062	Modulatio
C 35	6	100.0	10	6	BD167218	Human liv
C 36	6	100.0	10	6	BD225356	Compositi
C 37	6	100.0	11	6	AR016034	Sequence
C 38	6	100.0	11	6	AR026486	Sequence
C 39	6	100.0	11	6	AR026487	Sequence
C 40	6	100.0	11	6	AR059195	Sequence
C 41	6	100.0	11	6	AR075506	Sequence
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ALIGNMENTS

RESULT 1  
AX055801/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX055801  
Sequence 5 from Patent WO0073420.  
AX055801  
AX055801.1 GI:12228914  
synthetic construct  
artificial construct  
1 (bases 1 to 6)  
Hahn, W.C. and Weinberg, R.A.  
Creation of human tumorigenic cells and uses therefor  
Patent: WO 0073420-A 5 07-DEC-2000;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER

Pred. No. is the number of results predicted by chance to have a

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  Db 6 TTAGGG 1

RESULT 2
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  DEFINITION Sequence 10 from Patent WO0074667.
  ACCESSION  AX058275
  VERSION     AX058275.1 GI:12310774
  KEYWORDS   .
  SOURCE      synthetic construct
  ORGANISM    synthetic construct
               artificial sequences.
  REFERENCE  1
  AUTHORS    Au, J.L. and Wientjes, G.
  TITLE      Compositions active in telomere damage comprising a taxane and
               telomerase inhibitor
  JOURNAL    Patent: WO 0074667-A 10 14-DEC-2000;
               Au, Jessie L.S. (US) ; Wientjes, Guillaume (US)
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  DEFINITION Sequence 49 from Patent WO0144465.
  ACCESSION  AX175285
  VERSION     AX175285.1 GI:14598653
  KEYWORDS   .
  SOURCE      synthetic construct
  ORGANISM    synthetic construct
               artificial sequences.
  REFERENCE  1
  AUTHORS    Phillips, N.C. and Pillon, M.C.
  TITLE      Therapeutically useful synthetic oligonucleotides
  JOURNAL    Patent: WO 0144465-A 49 21-JUN-2001;
               Bioniche Life Sciences Inc. (CA)
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RESULT 4
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  DEFINITION Sequence 11 from Patent WO0174342.
  ACCESSION  AX268763
  VERSION     AX268763.1 GI:16541835
  KEYWORDS   .
  SOURCE      synthetic construct
  ORGANISM    synthetic construct
               artificial sequences.
  REFERENCE  1
  AUTHORS    Gilchrist, B.A., Yaar, M. and Eller, M.
  TITLE      Use of locally applied dna fragments
  JOURNAL    Patent: WO 0174342-A 11 11-OCT-2001;
               TRUSTEES OF BOSTON UNIVERSITY (US)
  FEATURES   1..6
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               /mol_type="genomic DNA"
               /db_xref="taxon:32630"
               /note="Synthetic DNA Fragment"

ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 7.2e+09;
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  QY 1 TTAGGG 6
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RESULT 5
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  ACCESSION  AX268764
  VERSION     AX268764.1 GI:16541836
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  SOURCE      synthetic construct
  ORGANISM    synthetic construct
               artificial sequences.
  REFERENCE  1
  AUTHORS    Gilchrist, B.A., Yaar, M. and Eller, M.
  TITLE      Use of locally applied dna fragments
  JOURNAL    Patent: WO 0174342-A 12 11-OCT-2001;
               TRUSTEES OF BOSTON UNIVERSITY (US)
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  QY 1 TTAGGG 6
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  Db 6 TTAGGG 1

FEATURES
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RESULT 6
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LOCUS      BD230086               8 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Method for making complementary oligonucleotide tag sets.
ACCESSION  BD230086
VERSION    BD230086.1 GI:33039856
KEYWORDS  JP 2002528137-A/3.
SOURCE    synthetic construct
ORGANISM  synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 8)
           Williams,S.R., Kirchner,J.J. and Dubridge,R.B.
           Method for making complementary oligonucleotide tag sets
           Patent: JP 2002528137-A 3 03-SEP-2002;
           LYNX THERAPEUTICS INC
COMMENT    OS Artificial Sequence
           PN JP 2002528137-A/3
           PD 03-SEP-2002
           PF 01-NOV-1999 JP 2000579783
           PR 02-NOV-1998 US 60/106662
           PI STEVEN R WILLIAMS,JAMES J KIRCHNER,ROBERT B DUBRIDGE PC
           C12N15/09,C12N15/09,C12N11/00,C12Q1/68,C12N15/00,C12N15/00 CC
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FEATURES   FH Key      Location/Qualifiers
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Query Match      100.0%; Score 6; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.4e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      3 TTAGGG 8

RESULT 7
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LOCUS      BD071049               8 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION  BD071049
VERSION    BD071049.1 GI:22616652
KEYWORDS  JP 2001517929-A/15.
SOURCE    unidentified
ORGANISM  unidentified
           unclassified.
REFERENCE  1 (bases 1 to 8)
           Shay,J.W., Wright,W.E., Piatsyzek,M.A., Corey,D. and Norton,J.C.
           Modulation of mammalian telomerase by peptide nucleic acids
           Patent: JP 2001517929-A 15 09-OCT-2001;
           GERON CORP
COMMENT    OS Unidentified
           PN JP 2001517929-A/15
           PD 09-OCT-2001
           PF 09-APR-1997 JP 1997536487
           PR 09-APR-1996 US 08/630019
           PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
           PI COREY,
           PI JAMES C NORTON
           PC C07K14/00,A61K38/16,C12Q1/68
           CC Strandedness: Single;
           CC Topology: Linear;
           CC /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
           linkages are replaced by N-(2-aminoethyl)glycine units linked
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Best Local Similarity 100.0%; Pred. No. 5.4e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      3 TTAGGG 8

RESULT 8
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LOCUS      BD071063               8 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION  BD071063
VERSION    BD071063.1 GI:22616666
KEYWORDS  JP 2001517929-A/29.
SOURCE    unidentified
ORGANISM  unidentified
           unclassified.
REFERENCE  1 (bases 1 to 8)
           Shay,J.W., Wright,W.E., Piatsyzek,M.A., Corey,D. and Norton,J.C.
           Modulation of mammalian telomerase by peptide nucleic acids
           Patent: JP 2001517929-A 29 09-OCT-2001;
           GERON CORP
COMMENT    OS Unidentified
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           PD 09-OCT-2001
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           PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
           PI COREY,
           PI JAMES C NORTON
           PC C07K14/00,A61K38/16,C12Q1/68
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DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION  BD071063
VERSION    BD071063.1 GI:22616666
KEYWORDS  JP 2001517929-A/29.
SOURCE    unidentified
ORGANISM  unidentified
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REFERENCE  1 (bases 1 to 8)
           Shay,J.W., Wright,W.E., Piatsyzek,M.A., Corey,D. and Norton,J.C.
           Modulation of mammalian telomerase by peptide nucleic acids
           Patent: JP 2001517929-A 29 09-OCT-2001;
           GERON CORP
COMMENT    OS Unidentified
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           PF 09-APR-1997 JP 1997536487
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           PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
           PI COREY,
           PI JAMES C NORTON
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 AUTHORS Modulation of mammalian telomerase by peptide nucleic acids  
 TITLE Patent: JP 2001517929-A 33 09-OCT-2001;  
 JOURNAL GERON CORP  
 COMMENT OS Unidentified  
 PN JP 2001517929-A/33  
 PD 09-OCT-2001  
 PF 09-APR-1997 JP 1997536487  
 PR 09-APR-1996 US 08/630019  
 PI JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID  
 PI COREY,  
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 DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.  
 ACCESSION BD071050  
 VERSION BD071050.1 GI:22616653  
 KEYWORDS JP 2001517929-A/16.  
 SOURCE unidentified  
 ORGANISM unidentified  
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 REFERENCE Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.  
 AUTHORS Modulation of mammalian telomerase by peptide nucleic acids  
 TITLE Patent: JP 2001517929-A 16 09-OCT-2001;  
 JOURNAL GERON CORP  
 COMMENT OS Unidentified

PN JP 2001517929-A/16  
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 PI JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID  
 PI COREY,  
 PI JAMES C NORTON  
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 DEFINITION Sequence 10 from patent US 5856096.  
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 VERSION AR026485.1 GI:5937325  
 KEYWORDS Unknown.  
 SOURCE Unclassified.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.  
 TITLE Rapid and sensitive assays for detecting and distinguishing between  
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 JOURNAL Patent: US 5856096-A 10 05-JAN-1999;  
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 ACCESSION BD238638  
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 KEYWORDS JP 2002534056-A/56.  
 SOURCE Homo sapiens (human)

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 56 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/56
PD 15-OCT-2002
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PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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G01N37/00,
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239195
VERSION BD239195.1 GI:33048965
KEYWORDS JP 2002534056-A/613.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 613 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
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PD 15-OCT-2002
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ACCESSION BD238940
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REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 358 15-OCT-2002;
GENZYME CORP
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PN JP 2002534056-A/358
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240276
VERSION BD240276.1 GI:33050046
KEYWORDS JP 2002534056-A/1694.
SOURCE Homo sapiens (human)
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1 (bases 1 to 10)
Robert, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1694 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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## SUMMARIES

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3	6	100.0	6	4 AAS14916	Aas14916 Melanogen
4	6	100.0	6	4 AAS14915	Aas14915 Melanogen
5	6	100.0	6	6 ABN73654	Abn73654 Bovine em
6	6	100.0	6	8 ACD25830	Acd25830 Telomere
7	6	100.0	6	8 ACD25831	Acd25831 Telomere
8	6	100.0	7	1 AAN91439	Aan91439 Telomere
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13	6	100.0	8	3 AAA37572	Aaa37572 PNA seque
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17	6	100.0	9	2 AAT89240	Aat89240 Peptide n
18	6	100.0	9	2 AAT93240	Aat93240 Telomerases
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## ALIGNMENTS

## RESULT 1

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AC AAT05734;  
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DT 01-FEB-1996 (first entry)  
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DE Telomerase oligonucleotide substrate #1.  
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KW Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;  
KW transplplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.  
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OS Synthetic.  
XX  
EN WO9513383-A1.  
XX  
PD 18-MAY-1995.  
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PF 10-NOV-1994; 94WO-US013130.  
XX  
PR 12-NOV-1993; 93US-00151477.  
PR 12-NOV-1993; 93US-00153051.  
XX (GERO-) GERON CORP.  
XX (TEXA) UNIV TEXAS SYSTEM.  
PI Shay J, West MD, Wright WE;  
XX WPI; 1995-224051/29.  
XX  
PT Increasing telomere length in cells - to increase proliferative capacity  
PT and therefore delay cellular senescence, useful in cell therapy and  
PT transplplantation.  
XX  
PS Claim 12; Page 29; 38pp; English.  
XX  
CC Oligonucleotides AAT05734-7 are examples of telomerase substrates used to  
CC increase the proliferative capacity of normal cells that express  
CC telomerase activity. The oligonucleotides allow an increase in length of  
CC telomeres in normal cells and in hybrids of normal and immortalised  
CC cells. The increase in telomere length extends the capacity of cells to  
CC replicate, esp. those treated ex vivo and used for transplantation  
CC techniques e.g. cell therapy, for the treatment of AIDS, anaemia,  
CC leukaemia or lymphoma

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Aax22183 Random am  
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Aaz85770 Metastati  
Aaz85516 Metastati

SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 6; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TTAGGG 6  
 |||||  
 Db 1 TTAGGG 6

RESULT 2  
 AAX80998  
 ID AAX80998 standard; DNA; 6 BP.  
 XX AC  
 XX AAX80998;  
 DT 13-SEP-1999 (first entry)  
 XX DE  
 XX Telomeric repeat sequence.  
 XX KW  
 KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;  
 KW immunogen; enzyme; telomerase-mediated DNA replication; human; ss.  
 XX OS  
 XX Homo sapiens.  
 XX PN  
 PN WO927113-A1.  
 XX PD  
 PD 03-JUN-1999.  
 XX PF  
 PF 25-NOV-1998; 98WO-US025211.  
 XX PR  
 PR 26-NOV-1997; 97US-00979742.  
 XX PR  
 PR 16-MAR-1998; 98US-00042460.  
 XX XX  
 XX (GERO-) GERON CORP.  
 PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
 XX PI  
 PI Morin GB, Allsopp R, Depinho R, Greenberg R;  
 XX XX  
 XX WPI; 1999-347722/29.  
 XX PT  
 PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and  
 XX PT  
 PT nucleic acids.  
 XX PS  
 PS Disclosure; Page 62; 135pp; English.  
 XX CC  
 CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)  
 CC enzyme. Compositions containing mTERT can be used in telomere length  
 CC assays. Isolated mTERT is useful as an immunogen for the production of  
 CC monoclonal or polyclonal antibodies. The method is useful for assessing  
 CC the degree of purification and identification of new mTERT species, such  
 CC as an mTERT allele, homolog or isoform, or to screen for modulators  
 CC (antagonists and agonists) of telomerase-mediated DNA replication.  
 CC Antagonists and agonists of mTERT can be used to modify the activity of  
 CC other telomerase enzymes such as human TERT (hTERT)  
 XX SQ  
 SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 6; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TTAGGG 6  
 |||||  
 Db 1 TTAGGG 6

RESULT 3  
 AAS14916/c  
 ID AAS14916 standard; DNA; 6 BP.  
 XX AC  
 XX AAS14916;

14-FEB-2002 (first entry)  
 Melanogenesis associated oligonucleotide #12.  
 Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 conjunctivitis; allergic rhinitis; vitiligo; ss.  
 Synthetic.  
 WO200174342-A2.  
 11-OCT-2001.  
 30-MAR-2001; 2001WO-US010162.  
 31-MAR-2000; 2000US-00540843.  
 (UYBO-) UNIV BOSTON.  
 Gilchrest BA, Year M, Eller M;  
 WPI; 2001-626338/72.  
 Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 carcinoma, using specific oligonucleotides that mimic the effects of  
 ultra-violet light.  
 Claim 1; Page 37; 74pp; English.  
 The invention describes inhibition of mammalian epithelial cell  
 proliferation by treating cells with at least one oligonucleotide, or its  
 fragment. The compounds, which have cytostatic, anti-allergic, anti-  
 inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 DNA repair processes (or a protective response to later exposure to  
 radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 or a tumour necrosis factor inhibitor. Probably they mimic products of  
 DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 pathway, resulting in transient arrest of cell growth, allowing more time  
 for DNA repair to occur before cell division takes place. The method is  
 especially used to treat carcinoma but may also be used to: treat other  
 hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 allergically mediated inflammation (atopic or contact dermatitis,  
 allergic rhinitis and conjunctivitis); prevent or reduce melanin production  
 cells caused by radiation or chemicals; increase melanin production  
 (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 promote apoptosis in epithelial cells that contain damaged DNA. Also  
 oligonucleotides that contain non-hydrolyzable backbones are used to  
 inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 sequence is melanogenesis associated oligonucleotide #12, the reverse  
 complementary sequence of AAS149015, a truncated version of the sequence  
 representing the telomere over-hang sequence (AAS14909), described in the  
 method of the invention  
 Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 6; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TTAGGG 6  
 |||||  
 Db 6 TTAGGG 1

RESULT 4  
 AAS14915

AA514915 standard; DNA; 6 BP.  
AA514915;  
14-FEB-2002 (first entry)  
Melanogenesis associated oligonucleotide #11.  
Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
tumour necrosis factor inhibitor; photocaging; hyperproliferative disease;  
carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
conjunctivitis; allergic rhinitis; vitiligo; ss.  
Synthetic.  
WO200174342-A2.  
11-OCT-2001.  
30-MAR-2001; 2001WO-US010162.  
31-MAR-2000; 2000US-00540843.  
(UYBO-) UNIV BOSTON.  
Gilchrest BA, Yaar M, Eller M;  
WPI; 2001-626338/72.  
Inhibiting proliferation of epithelial cells, useful e.g. for treating  
carcinoma, using specific oligonucleotides that mimic the effects of  
ultra-violet light.  
Claim 1; Page 37; 74pp; English.  
The invention describes inhibition of mammalian epithelial cell  
proliferation by treating cells with at least one oligonucleotide, or its  
fragment. The compounds, which have cytostatic, anti-allergic, anti-  
inflammatory, dermatological, ophthalmological, anti-psoriatic and  
immunosuppressive activities, function as 'ultra-violet mimics' to induce  
DNA repair processes (or a protective response to later exposure to  
radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
or a tumour necrosis factor inhibitor. Probably they mimic products of  
DNA damage, or processed DNA-damage intermediates, by inducing the p53  
pathway, resulting in transient arrest of cell growth, allowing more time  
for DNA repair to occur before cell division takes place. The method is  
especially used to treat carcinoma but may also be used to: treat other  
hyperproliferative states (e.g. psoriasis or precancerous conditions);  
reduce photocaging, oxidative stress or damage; prevent skin cancer; treat  
allergically mediated inflammation (atopic or contact dermatitis,  
allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
cells caused by radiation or chemicals; increase melanin production  
(pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
promote apoptosis in epithelial cells that contain damaged DNA. Also  
oligonucleotides that contain non-hydrolyzable backbones are used to  
inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
sequence is melanogenesis associated oligonucleotide #11, a truncated  
version of the sequence representing the telomere over-hang sequence  
(AA514909) and one of the oligonucleotides used to inhibit mammalian  
epithelial cell proliferation, described in the method of the invention  
Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 6; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTAGGG 6  
Db 1 TTAGGG 6  
Telomere repeat unit.  
Telomere; ds; cytostatic; human; antipsoriatic; dermatological;

RESULT 5  
ABN73654  
ID ABN73654 standard; cDNA; 6 BP.  
XX  
AC ABN73654;  
XX  
DT 03-JUL-2002 (first entry)  
XX  
DE Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 1.  
XX  
KW Bovine; Bos taurus; EST; expressed sequence tag; totipotence;  
KW development; gene; ss.  
XX  
OS Bos taurus.  
XX  
FN WO200194550-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 07-JUN-2001; 2001WO-US018576.  
XX  
PR 07-JUN-2000; 2000US-0209874P.  
PR 06-JUN-2001; 2001US-00876143.  
XX  
PA (INFI-) INFIGEN INC.  
XX  
PI Eilertsen KJ, Pfister-Genskow M, Childs L;  
XX  
DR WPI; 2002-351289/38.  
XX  
PT An expressed sequence tag (EST), the expression of which, or its  
PT complementary sequence, in a cell identifies the cell as a  
PT developmentally competent or incompetent cell.  
XX  
PS Example 16; Page 210; 584pp; English.  
XX  
CC The present invention describes an expressed sequence tag (EST), where  
CC the EST is an isolated, enriched, or purified nucleic acid sequence  
CC representing all or part of a gene, the expression of which, or its  
CC complementary sequence, in a cell identifies the cell as a  
CC developmentally competent or incompetent cell. Molecules which induce  
CC developmental competence in a cell line are useful for inducing  
CC totipotence in one or more cells. Molecules which induce developmental  
CC incompetence in a cell line are useful for preventing a full term  
CC pregnancy in an animal and inhibiting totipotence. The molecules are also  
CC useful for treating a disease in an animal by inducing development of one  
CC or more cells of the animal into a specific cell type. The present  
CC sequence represents a bovine EST which is given in the exemplification of  
CC the present invention  
XX  
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 6; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTAGGG 6  
Db 1 TTAGGG 6  
RESULT 6  
ACD25830  
ID ACD25830 standard; DNA; 6 BP.  
XX  
AC ACD25830;  
XX  
DT 08-SEP-2003 (first entry)  
XX  
DE Telomere repeat unit.  
XX  
KW Telomere; ds; cytostatic; human; antipsoriatic; dermatological;

KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;  
KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;  
KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;  
KW gp-1100; hyperproliferative disorder; spongiosis; blistering;  
KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;  
KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;  
KW atopic dermatitis; breast cancer; lung cancer; liver cancer;  
KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;  
KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;  
KW stomach cancer; thyroid cancer.  
XX  
XX  
OS Homo sapiens.  
XX  
XX US2003032610-A1.  
XX  
XX 13-FEB-2003.  
XX  
XX 12-APR-2002; 2002US-00122630.  
XX  
XX 03-JUN-1996; 96WO-US008386.  
XX 26-MAR-1998; 98US-00048927.  
XX 31-MAR-2000; 2000US-00540843.  
XX 30-MAR-2001; 2001WO-US010162.  
XX  
XX (GILC/) GILCHREST B A.  
XX PA (ELLE/) ELLER M S.  
XX PA (YAAR/) YAAR M.  
XX  
XX Gilchrest BA, Eller MS, Yaar M;  
XX WPI; 2003-512221/48.  
XX  
XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,  
XX PT by administering composition having oligonucleotides that share sequence  
XX PT identity with human telomere overhang repeat.  
XX  
XX Claim 44; Page 9; 65pp; English.  
XX  
XX The invention relates to inhibiting growth of cancer cells, which is  
XX independent of presence or activity of telomerase in cells, not requiring  
XX the presence or activity of p53 normal function in cells, or resulting in  
XX S-phase arrest in cells, and inducing apoptosis in cancer cells,  
XX involving administering a composition comprising oligonucleotides which  
XX share at least 50% sequence identity with human telomere overhang repeat,  
XX (TTAGG)n. The composition may contain 2 of the oligonucleotides for their  
XX contiguous portion) and is used in a method inhibiting proliferation of  
XX epithelial cells in a mammal or preventing/reducing DNA damage in cells  
XX of a mammal, where the DNA damage is caused by radiation or DNA-damaging  
XX chemicals. The method is useful for inhibiting growth of cancer cells  
XX (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,  
XX squamous cell carcinoma), for inducing apoptosis in cancer cells in  
XX human, promoting differentiation of malignant cells in a mammal,  
XX enhancing the expression of one or more surface antigens (e.g. MART-1,  
XX tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer  
XX cells (especially melanoma cells) in a human and for treatment of other  
XX hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis  
XX in the skin of a mammal, skin cancer in a human with xeroderma  
XX pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or  
XX basal cell carcinoma) and for treating or preventing pre-cancerous  
XX conditions affecting epithelial cells (such as psoriasis and atopic  
XX dermatitis) and also the types of cancers of breast, lung, liver,  
XX prostate, pancreatic, ovarian, bladder, uterine, colon, brain,  
XX oesophagus, stomach, and thyroid. The present sequence is the telomere  
XX repeat unit sequence  
XX  
XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;  
XX SQ

Query Match 100.0%; Score 6; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
|||||

Db 1 TTAGGG 6  
RESULT 7  
ACD25831/C  
ID ACD25831 standard; DNA; 6 BP.  
XX  
XX ACD25831;  
XX AC  
XX 08-SEP-2003 (first entry)  
XX DT  
XX XX  
XX DE  
XX XX  
XX Telomere repeat unit (complement).  
XX  
XX Telomere; ds; cytostatic; human; antipsoriatic; dermatological;  
KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;  
KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;  
KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;  
KW gp-1100; hyperproliferative disorder; spongiosis; blistering;  
KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;  
KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;  
KW atopic dermatitis; breast cancer; lung cancer; liver cancer;  
KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;  
KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;  
KW stomach cancer; thyroid cancer.  
XX  
XX Homo sapiens.  
XX OS  
XX XX  
XX PN US2003032610-A1.  
XX PD 13-FEB-2003.  
XX  
XX 12-APR-2002; 2002US-00122630.  
XX PF  
XX 03-JUN-1996; 96WO-US008386.  
XX PR 26-MAR-1998; 98US-00048927.  
XX PR 31-MAR-2000; 2000US-00540843.  
XX PR 30-MAR-2001; 2001WO-US010162.  
XX  
XX (GILC/) GILCHREST B A.  
XX PA (ELLE/) ELLER M S.  
XX PA (YAAR/) YAAR M.  
XX  
XX Gilchrest BA, Eller MS, Yaar M;  
XX WPI; 2003-512221/48.  
XX  
XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,  
XX PT by administering composition having oligonucleotides that share sequence  
XX PT identity with human telomere overhang repeat.  
XX  
XX Claim 44; Page 18; 65pp; English.  
XX  
XX The invention relates to inhibiting growth of cancer cells, which is  
XX independent of presence or activity of telomerase in cells, not requiring  
XX the presence or activity of p53 normal function in cells, or resulting in  
XX S-phase arrest in cells, and inducing apoptosis in cancer cells,  
XX involving administering a composition comprising oligonucleotides which  
XX share at least 50% sequence identity with human telomere overhang repeat,  
XX (TTAGG)n. The composition may contain 2 of the oligonucleotides for their  
XX contiguous portion) and is used in a method inhibiting proliferation of  
XX epithelial cells in a mammal or preventing/reducing DNA damage in cells  
XX of a mammal, where the DNA damage is caused by radiation or DNA-damaging  
XX chemicals. The method is useful for inhibiting growth of cancer cells  
XX (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,  
XX squamous cell carcinoma), for inducing apoptosis in cancer cells in  
XX human, promoting differentiation of malignant cells in a mammal,  
XX enhancing the expression of one or more surface antigens (e.g. MART-1,  
XX tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer  
XX cells (especially melanoma cells) in a human and for treatment of other  
XX hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis  
XX in the skin of a mammal, skin cancer in a human with xeroderma  
XX pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or  
XX basal cell carcinoma) and for treating or preventing pre-cancerous

CC conditions affecting epithelial cells (such as psoriasis and atopic dermatitis) and also the types of cancers of breast, lung, liver, CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain, CC oesophagus, stomach, and thyroid. The present sequence is the complement CC of telomere repeat unit sequence found to be less active in melanogenesis XX  
SQ Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 6; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
Db 6 TTAGGG 1

## RESULT 8

AAN91439/c  
ID AAN91439 standard; DNA; 7 BP.

XX AC AAN91439;

XX DT 25-MAR-2003 (revised)  
XX DT 22-FEB-1990 (first entry)

XX DE Telomere of Arabidopsis thaliana.

XX KW Telomere; Arabidopsis thaliana; vector; artificial chromosomes;  
XX KW tandem repeat.

XX OS Arabidopsis thaliana.

XX PN WO8909219-A.

XX PD 05-OCT-1989.

XX PF 27-FEB-1989; 89WO-US000795.

XX PR 24-MAR-1988; 88US-00172467.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Richards E, Ausubel FM;

XX DR WPI; 1989-309497/42.

XX PT New recombinant DNA contg. eukaryotic telomere esp. from higher plant -  
XX PT useful as vector for specific genes and maintained in nucleus as  
XX PT independent replicating molecule.

XX PS Claim 28; Page 50; 65pp; English.

XX CC Tandem repeats (1-1000) of the telomere are used in a vector for  
XX CC expressing specific genes in plants. They provide 'artificial  
XX CC chromosomes' which are maintained in the nucleus, so are not subjected to  
XX CC variable expression due to integration-position effects. They allow the  
XX CC integration of very foreign DNA without host range limitations. The  
XX CC telomere opt. contains variant repeats of CTCAAA. The telomere is pref.  
XX CC the pAT4 plasmid (ATCC 67577). (Updated on 25-MAR-2003 to correct PA  
XX CC field.)

XX SQ Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 6; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
Db 6 TTAGGG 1

## RESULT 9

AAN91442/c

ID AAN91442 standard; DNA; 7 BP.

XX AC AAN91442;

XX DT 25-MAR-2003 (revised)  
XX DT 22-FEB-1990 (first entry)

XX DE Variant of Arabidopsis thaliana telomere.

XX KW Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;  
XX KW tandem repeat.

XX OS Arabidopsis thaliana.

XX PN WO8909219-A.

XX PD 05-OCT-1989.

XX PF 27-FEB-1989; 89WO-US000795.

XX PR 24-MAR-1988; 88US-00172467.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Richards E, Ausubel FM;

XX DR WPI; 1989-309497/42.

XX PT New recombinant DNA contg. eukaryotic telomere esp. from higher plant -  
XX PT useful as vector for specific genes and maintained in nucleus as  
XX PT independent replicating molecule.

XX PS Claim 35; Page 50; 65pp; English.

XX CC The DNA is a variant of the telomere of the pAT4 plasmid (ATCC 67577).  
XX CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 6; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
Db 6 TTAGGG 1

## RESULT 10

AAQ97993

ID AAQ97993 standard; DNA; 8 BP.

XX AC AAQ97993;

XX DT 25-MAR-2003 (revised)  
XX DT 19-OCT-1995 (first entry)

XX DE Peptide nucleic acid oligomer targetting HIV gene.

XX KW Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;  
XX KW antiviral; antisense; triple helix; ss.

XX OS Synthetic.

XX PH Key misc\_feature Location/Qualifiers  
XX FT 1. .8

XX FT /note= "at least one (and preferably all) of the backbone  
XX FT subunits are composed of N-acetyl N-(2-aminoethyl)glycine  
XX FT peptide residues, the nucleobase being attached  
XX FT covalently to the acetyl group and the peptide linkage

being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"

FT WO9504068-A1.  
 FT 09-FEB-1995.  
 FT 28-JUL-1994; 94WO-US008517.  
 FT 29-JUL-1993; 93US-00099718.  
 FT (ISIS-) ISIS PHARM INC.  
 FT Ecker DJ;  
 FT WPI; 1995-082179/11.  
 FT Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid  
 FT sub-unit - binds in complementary manner to DNA and RNA, and useful for  
 FT modulating HIV viral activity, e.g. in treating AIDS.  
 PS Claim 2; Page 176; 186pp; English.  
 CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist  
 CC of naturally occurring nucleobases covalently bound to a polyamide  
 CC backbone and (b) hybridise to the translation initiation AUG region, 5'  
 CC untranslated region (5' UTR), 3' untranslated region (3' UTR), splice  
 CC junctions or coding sequence of a human immunodeficiency virus gene  
 CC chosen from env, gag, pol, rev and tat. The PNAs can be used to target  
 CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene  
 CC regulation moieties. They have utility as gene-targeted drugs for  
 CC modulating HIV processes. Hence they can be used to treat AIDS and other  
 CC viral infections. They are also useful in diagnostic applications and as  
 CC research tools. PNA oligomers have high affinity for complementary single  
 CC stranded DNA. They are also able to form triple helices in which a first  
 CC PNA strand binds with RNA or ssDNA and a second PNA strand binds with the  
 CC resulting double helix or with the first PNA strand. The PNAs possess no  
 CC significant charge and are water soluble, which facilitates cellular  
 CC uptake. Further, since they contain amides of non-biological amino acids,  
 CC they are biostable and resistant to enzymatic degradation by proteases.  
 CC The present sequence is a specifically claimed PNA sequence (represented  
 CC by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 8 BP; 1 A; 0 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 6; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+08; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTAGGG 6  
 Db 1 TTAGGG 6  
 RESULT 11  
 AAT89239  
 ID AAT89239 standard; DNA; 8 BP.  
 AC AAT89239;  
 XX 12-MAY-1998 (first entry)  
 DE Peptide nucleic acid 14, targeted to mammalian telomerase.  
 XX Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;  
 KW inhibitor; ss.  
 KW Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH modified\_base 1. .8  
 FT

/\*tag= a  
 /note= "Sugar-phosphate backbone has been replaced by a  
 peptide backbone"  
 PN WO9738013-A1.  
 XX 16-OCT-1997.  
 XX 09-APR-1997; 97WO-US005931.  
 XX 09-APR-1996; 96US-00630019.  
 XX (GERO-) GERON CORP.  
 XX Shay JW, Wright WE, Piatyszek MA, Corey D, Norton JC;  
 XX WPI; 1997-512647/47.  
 XX New peptide nucleic acids hybridising to mammalian telomerase RNA - used  
 XX to inhibit telomerase, for treating tumours and other proliferative  
 XX diseases, also for diagnosis.  
 PS Claim 9; Page 59; 76pp; English.  
 CC This sequence is a novel peptide nucleic acid (PNA), which acts as an  
 CC inhibitor of mammalian, preferably human, telomerase. The PNAs hybridise  
 CC specifically to an RNA component of mammalian telomerase, and include the  
 CC sequence GGG for specific hybridisation to the template region of this  
 CC component. PNAs can be used as probes to detect the RNA component of  
 CC mammalian telomerase and as inhibitors of telomerase activity, especially  
 CC in the treatment of cancer  
 XX  
 SQ Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 6; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+08; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTAGGG 6  
 Db 2 TTAGGG 7  
 RESULT 12  
 AAA37558  
 ID AAA37558 standard; DNA; 8 BP.  
 AC AAA37558;  
 XX 15-AUG-2000 (first entry)  
 DE PNA sequence #15 used to inhibit telomerase activity.  
 XX Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 KW paternity testing; ss.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH misc\_feature 1. .8  
 FT /\*tag= a  
 FT /note= "Peptide nucleic acid molecule, where N-(2-  
 FT aminoethyl)glycine units are linked to nucleotide bases  
 FT via glycine amino N through a methylenecarbonyl linker"  
 XX  
 PN US6046307-A.  
 XX 04-APR-2000.  
 XX 09-APR-1997; 97US-00838545.  
 XX

PR 09-APR-1996; 96US-00630019.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Wright WE, Piattyszek MA, Shay JW, Norton JC, Corey DR;  
 XX  
 DR WPI; 2000-292432/25.  
 XX  
 PT New peptide nucleic acid (PNA) compounds that inhibit telomerase activity  
 PT in mammalian cells is useful as probes to detect the RNA component of a  
 PT mammalian telomerase.  
 XX  
 PS Claim 6; Col 71; 45pp; English.  
 XX  
 CC The present sequence represents a peptide nucleic acid molecule which  
 CC hybridizes to the mRNA component of mammalian telomerase, and inhibits  
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 CC synthesizes one strand of the telomeric DNA, using as a template an 11  
 CC nucleotide sequence contained within the RNA component of the enzyme. The  
 CC invention relates to PNA molecules having a sequence of no more than 25  
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 CC backbone increases the melting temperature of associating strands,  
 CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance of degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism or telomerase  
 CC activity, in combination with antineoplastic and other cytotoxic or  
 CC cytosstatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification  
 CC of individuals, e.g. paternity testing, based on hTR gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 CC probes to detect the RNA component of a mammalian telomerase and as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component  
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 SQ Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 6; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTAGGG 6  
 Db |||||  
 2 TTAGGG 7  
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 ID AAA37572 standard; DNA; 8 BP.  
 AC AAA37572;  
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 XX 15-AUG-2000 (first entry)  
 DE PNA sequence #30 used to inhibit telomerase activity.  
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 KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 KW paternity testing; ss.  
 XX  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT misc\_feature 1..8  
 FT /\*tag= a  
 FT /note= "Peptide nucleic acid molecule, where N-(2-  
 FT aminoethyl)glycine units are linked to nucleotide bases  
 FT via glycine amino N through a methylene-carbonyl linker"  
 XX  
 PN US6046307-A.  
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 PD 04-APR-2000.  
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 PF 09-APR-1997; 97US-00838545.  
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 PR 09-APR-1996; 96US-00630019.  
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 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Wright WE, Piattyszek MA, Shay JW, Norton JC, Corey DR;  
 XX  
 DR WPI; 2000-292432/25.  
 XX  
 PT New peptide nucleic acid (PNA) compounds that inhibit telomerase activity  
 PT in mammalian cells is useful as probes to detect the RNA component of a  
 PT mammalian telomerase.  
 XX  
 PS Example 2; Col 33; 45pp; English.  
 XX  
 CC The present sequence represents a peptide nucleic acid molecule which  
 CC hybridizes to the mRNA component of mammalian telomerase, and inhibits  
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 CC synthesizes one strand of the telomeric DNA, using as a template an 11  
 CC nucleotide sequence contained within the RNA component of the enzyme. The  
 CC invention relates to PNA molecules having a sequence of no more than 25  
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 CC backbone increases the melting temperature of associating strands,  
 CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance of degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism or telomerase  
 CC activity, in combination with antineoplastic and other cytotoxic or  
 CC cytosstatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification  
 CC of individuals, e.g. paternity testing, based on hTR gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 CC probes to detect the RNA component of a mammalian telomerase and as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component  
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 SQ Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 U; 0 Other;  
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 7 TTAGGG 2  
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 AAS15436  
 ID AAS15436 standard; DNA; 8 BP.  
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AC AAS15436;
XX
XX DT 14-FEB-2002 (first entry)
XX DE PNA 28 inhibiting human and mammalian telomerase activity.
XX
XX Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
KW human telomerase RNA component; hTR gene RFLP pattern; cancer;
KW inflammation; lymphoproliferative disease; autoimmune disease;
KW neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
KW human immunodeficiency virus; acquired immunodeficiency syndrome;
KW telomere metabolism; mutant; cytostatic; anti-inflammatory;
KW immunosuppressive; polyamide backbone; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
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FT /tag= a
FT /note= "This sequence is a peptide nucleic acid, i.e. it
FT contains a polyamide backbone instead of a deoxyribose
FT backbone"
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XX US6294650-B1.
XX
XX 25-SEP-2001.
XX
XX 08-JUL-1999; 99US-00349532.
XX
XX 09-APR-1996; 96US-00630019.
XX 09-APR-1997; 97US-00838545.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;
XX WPI; 2001-638024/73.
XX
XX New peptide nucleic acids that hybridizes to the RNA component of
XX mammalian telomerase, useful for treating or preventing cancer,
XX inflammation, lymphoproliferative diseases, autoimmune disease, or
XX neurodegenerative diseases.
XX
XX Claim 7; Col 73; 46pp; English.
XX
XX The present invention relates to peptide nucleic acids (PNAs), comprising
XX a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX mammalian cells by hybridising to the RNA component of mammalian
XX telomerase. The PNAs are useful as probes to detect the RNA component of
XX mammalian telomerase and as inhibitors of telomerase activity, or to
XX detect and/or quantitate polynucleotide having the human telomerase RNA
XX component (hTR) sequence, as well as in forensic identification of
XX individuals, such as paternity testing or identification of criminal
XX suspects or unknown descendants based on the hTR gene RFLP pattern. The
XX PNA can be further used for treating or preventing cancer, inflammation,
XX lymphoproliferative diseases, autoimmune disease, or neurodegenerative
XX diseases. The PNAs in combination with other pharmaceuticals (such as
XX antineoplastic or cytostatic agents) can be used for treating neoplasia,
XX hyperplasia, human immunodeficiency virus (HIV) infections, acquired
XX immunodeficiency syndrome (AIDS) and associated pathologies, and other
XX diseases characterised by abnormal telomere metabolism or telomerase
XX activity. The present sequence represents one of the PNA sequences of the
XX invention
XX
XX Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 6; DB 4; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 5.2e+08;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 TTAGGG 6
XX |||||

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CC antineoplastic or cytostatic agents) can be used for treating neoplasia,  
 CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired  
 CC immunodeficiency syndrome (AIDS) and associated pathologies, and other  
 CC diseases characterised by abnormal telomere metabolism or telomerase  
 CC activity. The present sequence represents one of the PNA sequences of the  
 CC invention. Note: The present sequence is given in the SEQ ID listing but  
 CC is not mentioned elsewhere in the patent  
 XX

SQ Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 2 Other;

Query Match 100.0%; Score 6; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.2e+08;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 TTAGGG 7

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 Job time : 89.043 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Perfect score: 6  
Sequence: 1 ttaggg 6

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Total number of hits satisfying chosen parameters: 2263564

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Listing first 45 summaries

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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6	100.0	6	9	US-09-817-387-29	Sequence 29, Appl
2	6	100.0	6	9	US-09-735-363A-49	Sequence 49, Appl
3	6	100.0	6	9	US-09-730-893-1	Sequence 1, Appl
4	6	100.0	6	10	US-09-940-173A-1	Sequence 1, Appl
5	6	100.0	6	13	US-09-907-279-2	Sequence 2, Appl
6	6	100.0	6	15	US-10-122-630-11	Sequence 11, Appl
7	6	100.0	6	15	US-10-122-630-11	Sequence 11, Appl
8	6	100.0	6	15	US-10-122-630-11	Sequence 11, Appl
9	6	100.0	6	15	US-10-122-633-11	Sequence 11, Appl
10	6	100.0	6	15	US-10-122-633-12	Sequence 12, Appl
11	6	100.0	6	15	US-10-255-535-8	Sequence 8, Appl
12	6	100.0	6	15	US-10-336-265-1	Sequence 1, Appl
13	6	100.0	6	15	US-10-336-265-3	Sequence 3, Appl
14	6	100.0	6	15	US-10-336-265-4	Sequence 4, Appl

15	6	100.0	6	15	US-10-336-265-64	Sequence 64, Appl	
16	6	100.0	6	15	US-10-232-927A-9	Sequence 9, Appl	
c	17	6	100.0	6	15	US-10-232-927A-27	Sequence 27, Appl
18	6	100.0	6	16	US-10-382-754B-3	Sequence 3, Appl	
19	6	100.0	6	16	US-10-355-388-3	Sequence 3, Appl	
20	6	100.0	6	17	US-10-181-823-13	Sequence 13, Appl	
21	6	100.0	6	17	US-10-705-531-15	Sequence 15, Appl	
22	6	100.0	6	17	US-10-705-531-16	Sequence 16, Appl	
23	6	100.0	7	9	US-09-730-893-6	Sequence 6, Appl	
24	6	100.0	7	10	US-09-940-173A-6	Sequence 6, Appl	
25	6	100.0	8	9	US-09-730-893-4	Sequence 4, Appl	
26	6	100.0	8	10	US-09-940-173A-4	Sequence 4, Appl	
27	6	100.0	8	15	US-10-336-265-58	Sequence 58, Appl	
c	28	6	100.0	9	US-09-728-574-19	Sequence 19, Appl	
29	6	100.0	10	13	US-10-325-810-527	Sequence 527, App	
30	6	100.0	10	14	US-10-033-145-56	Sequence 56, Appl	
31	6	100.0	10	14	US-10-033-145-358	Sequence 358, App	
32	6	100.0	10	14	US-10-033-145-613	Sequence 613, App	
33	6	100.0	10	14	US-10-033-145-1694	Sequence 1694, Ap	
34	6	100.0	10	15	US-10-044-692-294	Sequence 294, App	
35	6	100.0	10	15	US-10-044-539-294	Sequence 294, App	
36	6	100.0	10	15	US-10-390-045-41	Sequence 41, Appl	
37	6	100.0	10	15	US-10-330-627-92	Sequence 92, Appl	
c	38	6	100.0	10	15	US-10-330-627-1296	Sequence 1296, Ap
39	6	100.0	10	15	US-10-330-627-1297	Sequence 1297, Ap	
c	40	6	100.0	10	15	US-10-330-627-1298	Sequence 1298, Ap
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42	6	100.0	10	17	US-10-434-479-41	Sequence 41, Appl	
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44	6	100.0	11	10	US-09-835-370-63	Sequence 63, Appl	
c	45	6	100.0	11	10	US-09-249-155-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1  
US-09-817-387-29  
; Sequence 29, Application US/09817387  
; Patent No. US20010039263A1  
; GENERAL INFORMATION:  
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin  
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof  
; FILE REFERENCE: 101195-24  
; CURRENT APPLICATION NUMBER: US/09/817,387  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: DE 197 20 151.2  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 6  
; TYPE: DNA  
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; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: telomeric  
; OTHER INFORMATION: DNA of man  
US-09-817-387-29

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Best Local Similarity 100.0%; Pred. No. 7.9e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
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Db 1 TTAGGG 6

RESULT 2  
US-09-735-363A-49  
; Sequence 49, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:

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; APPLICANT: Pillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
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; Sequence 1, Application US/09730893
; Patent No. US20020107258A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: UTSG:679USC1
; CURRENT APPLICATION NUMBER: US/09/730,893
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/073,629
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 12
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-730-893-1

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Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
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; Sequence 1, Application US/09940173A
; Publication No. US20030040525A1
; GENERAL INFORMATION:
; APPLICANT: KERWIN, SEAN M.
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; APPLICANT: FEDOROFF, OLEG Y.
; APPLICANT: SALAZAR, MIGUEL
; APPLICANT: HURLEY, LAURENCE H.
; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
; FILE REFERENCE: G-QUADRUPLIX-INTERACTION COMPOUND
; CURRENT APPLICATION NUMBER: US/09/940,173A
; CURRENT FILING DATE: 2002-06-24
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; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/244,675
; PRIOR FILING DATE: 1999-04-02
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; Sequence 2, Application US/09907279
; Publication No. US20020068296A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Adam
; TITLE OF INVENTION: CATHODIC PROTECTION OF NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 11154.41USU1
; CURRENT APPLICATION NUMBER: US/09/907,279
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/218,959
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial oligonucleotide sequence
US-09-907-279-2

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QY      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 6
US-10-122-630-11
; Sequence 11, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
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; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
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; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
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; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
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Best Local Similarity 100.0%; Pred. No. 7.9e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTAGGG 6  
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; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaar, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
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; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-12

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.9e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||

Db 6 TTAGGG 1

## RESULT 8

US-10-122-633-11  
; Sequence 11, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaar, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-11

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.9e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||

Db 1 TTAGGG 6  
|||||

## RESULT 9

US-10-122-633-12/c  
; Sequence 12, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaar, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-12

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.9e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||

Db 6 TTAGGG 1  
|||||

```
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-3

Query Match      100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      6 TTAGGG 1

RESULT 13
US-10-336-265-4/c
; Sequence 4, Application US/10336265
; Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-336-265-4

Query Match      100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      6 TTAGGG 1

RESULT 14
US-10-336-265-63
; Sequence 63, Application US/10336265
; Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 6
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```
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-255-535-8

Query Match      100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 11
US-10-336-265-1
; Sequence 1, Application US/10336265
; Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-1

Query Match      100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTAGGG 6
Db      1 TTAGGG 6

RESULT 12
US-10-336-265-3/c
; Sequence 3, Application US/10336265
; Publication No. US20030148988A1
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-336-265-63

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred.No. 7.9e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||  
Db 1 TTAGGG 6

RESULT 15

US-10-336-265-64  
; Sequence 64, Application US/10336265  
; Publication No. US2003014988A1  
; GENERAL INFORMATION:  
; APPLICANT: Kool, Eric T.  
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for  
; FILE REFERENCE: 12665.0021.NFUS01  
; CURRENT APPLICATION NUMBER: US/10/336,265  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: US 60/345,056  
; PRIOR FILING DATE: 2002-01-04  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 64  
; LENGTH: 6  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-336-265-64

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 66.7%; Pred.No. 7.9e+08;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
:|  
Db 1 UAGGG 6

Search completed: August 11, 2004, 21:11:08  
Job time : 87.8495 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 16:50:49 ; Search time 718.258 Seconds  
(without alignments)  
249.455 Million cell updates/sec

Title: US-09-540-843-11  
Perfect score: 6  
Sequence: 1 ttaggg 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0  
Maximum DB seq length: 200

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estro:\*  
7: em\_estpl:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gsl:\*  
29: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	16	10	AW248958 2819454.3
2	6	100.0	19	28	AZ392246 IM0154G12
3	6	100.0	19	28	AZ422271 IM0200F10
4	6	100.0	19	28	AZ614760 IM0443A17

C	5	6	100.0	19	28	AZ826736
C	6	6	100.0	20	13	BQ593485
C	7	6	100.0	20	28	AZ345513
	8	6	100.0	20	28	AZ627174
	9	6	100.0	20	28	AZ662909
	10	6	100.0	20	28	AZ808291
C	11	6	100.0	20	28	AZ960008
C	12	6	100.0	20	29	TA158A03P
C	13	6	100.0	20	29	TA199G02Q
C	14	6	100.0	21	10	AW248826
C	15	6	100.0	21	10	AW248836
C	16	6	100.0	21	14	CF281817
C	17	6	100.0	21	28	AZ331625
C	18	6	100.0	21	28	AZ399400
C	19	6	100.0	21	28	AZ45481
C	20	6	100.0	21	28	AZ626594
C	21	6	100.0	21	28	AZ760907
C	22	6	100.0	21	28	AZ766315
C	23	6	100.0	21	28	AZ828389
C	24	6	100.0	21	28	AZ833919
C	25	6	100.0	21	28	AZ877328
C	26	6	100.0	22	9	AA954126
C	27	6	100.0	22	9	AA527213
C	28	6	100.0	22	14	D18745
C	29	6	100.0	22	28	AZ324747
C	30	6	100.0	22	28	AZ464647
	31	6	100.0	22	28	AZ483833
	32	6	100.0	22	28	AZ500414
C	33	6	100.0	22	28	AZ598320
C	34	6	100.0	22	28	AZ629501
	35	6	100.0	22	28	AZ666649
	36	6	100.0	22	28	AZ836104
C	37	6	100.0	22	28	AZ855118
C	38	6	100.0	23	9	AU258772
C	39	6	100.0	23	14	CA794240
C	40	6	100.0	23	28	AZ423815
	41	6	100.0	23	28	AZ465280
	42	6	100.0	23	28	AZ623979
	43	6	100.0	23	28	AZ817008
C	44	6	100.0	23	28	AZ979817
	45	6	100.0	23	28	BH857265

#### ALIGNMENTS

RESULT 1  
AW248958  
LOCUS  
DEFINITION  
ACCSSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW248958 16 bp mRNA linear EST 07-JAN-2000  
2819454.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819454 3',  
mRNA sequence.  
AW248958  
AW248958.1 GI:6591951  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819454.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LMNL) DNA Sequencing by: Berkeley MGC sequencing  
Project Clone Distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LMNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center  
Trimming: cross\_match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1CWI row: K column: 7  
High quality sequence stop: 15.

#### FEATURES

source  
Location/Qualifiers  
1..16  
/organism="Homo sapiens"  
/mol\_type="mrna"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819454"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MG3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 100.0%; Score 6; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 9 TTAGGG 14

RESULT 2  
AZ392246 19 bp DNA linear GSS 03-OCT-2000  
LOCUS IM0154G12R Mouse 10kb plasmid UGCLM library Mus musculus genomic  
DEFINITION clone UGCLM0154G12 R, genomic survey sequence.

ACCESSION AZ392246  
VERSION AZ392246.1 GI:10507234  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

#### ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0154 row: G column: 12

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

#### FEATURES

source  
Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0154G12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 14 TTAGGG 19

#### RESULT 3

AZ422271/c 19 bp DNA linear GSS 03-OCT-2000  
LOCUS IM0200F10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0200F10 R, genomic survey sequence.

ACCESSION AZ422271  
VERSION AZ422271.1 GI:10546284  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

#### ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0200 row: F column: 10

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

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FEATURES                                     Location/Qualifiers
source
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0200F10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match          100.0%; Score 6; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
   |||||
Db 8 TTAGGG 3

RESULT 4
AZ614760
LOCUS          19 bp DNA linear GSS 13-DEC-2000
DEFINITION    IM043A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0443A17 R, genomic survey sequence.
ACCESSION     AZ614760
VERSION       AZ614760.1 GI:11736950
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0443 row: A column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

```

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FEATURES                                     Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0443A17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match          100.0%; Score 6; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
   |||||
Db 4 TTAGGG 9

RESULT 5
AZ826736/c
LOCUS          19 bp DNA linear GSS 20-FEB-2001
DEFINITION    2M0102N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0102N07 R, genomic survey sequence.
ACCESSION     AZ826736
VERSION       AZ826736.1 GI:12996644
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: N column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

```

FEATURES  
source

Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0102N07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGClM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 17 TTAGGG 12

## RESULT 6

BQ593485/c  
LOCUS BQ593485 20 bp mRNA linear EST 06-DEC-2002  
DEFINITION S015529-024-026-P04-SP6 MPZ-ADIS-024-developing root Beta vulgaris cDNA clone 024-026-P04 5-PRIME, mRNA sequence.

ACCESSION BQ593485  
VERSION BQ593485.1 GI:26123068  
KEYWORDS EST.  
SOURCE Beta vulgaris

## ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

AUTHORS Drungowski, M., Stahl, D., Wruuck, W., Menze, A., O'Brien, J., Lehrach, H., and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

## COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: [weissshaar@piz-koeln.mpg.de](mailto:weissshaar@piz-koeln.mpg.de)

Insert Length: 20 Std Error: 0.00

Plate: 26 row: P column: 04

Seq primer: SP6; CATACGATTAGTGACTATAG.

## FEATURES

source

Location/Qualifiers  
1. .20

/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:193369"  
/db\_xref="taxon:161934"  
/clone="024-026-P04"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPZ-ADIS-024-developing root"  
/note="Vector: PCWVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

## ORIGIN

Query Match 100.0%; Score 6; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 18 TTAGGG 13

## RESULT 7

AZ345513/c

LOCUS AZ345513 20 bp DNA linear GSS 29-SEP-2000

DEFINITION IM0080J04F Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGClM0080J04 F, genomic survey sequence.

ACCESSION AZ345513

VERSION AZ345513.1 GI:10424750

KEYWORDS GSS

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunne@genetics.utah.edu](mailto:ddunne@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: J column: 04

Seq primer: CTTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGClM0080J04"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTAGGG 6  
| | | | |  
Db 13 TTAGGG 18

RESULT 9  
AZ662909  
LOCUS  
DEFINITION  
IM0542G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0542G17 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0542 row: G column: 17  
Seq primer: CGTTGTAACACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source  
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Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0542G17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTAGGG 6  
| | | | |  
Db 16 TTAGGG 11

RESULT 8  
AZ627174  
LOCUS  
DEFINITION  
IM0467010R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0467010 R, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0467 row: O column: 10  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

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1..20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0467010"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
 |||||  
 Db 7 TTAGGG 12

## RESULT 10

AZ808291  
 LOCUS  
 DEFINITION 20 bp DNA linear GSS 20-FEB-2001  
 clone UUGC2M0071D09 R, genomic survey sequence.

ACCESSION  
 AZ808291

VERSION  
 AZ808291.1 GI:12973320

KEYWORDS  
 GSS.

SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 20)

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D. Weiss,R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

plasmid inserts

## COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0071 row: D column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

## FEATURES

source

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0071D09"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
 |||||  
 Db 6 TTAGGG 11

## RESULT 11

AZ960008/c

LOCUS

DEFINITION 20 bp DNA linear GSS 27-APR-2001

clone UUGC2M0227G21 R, genomic survey sequence.

ACCESSION

AZ960008

VERSION

AZ960008.1 GI:13831235

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0227 row: G column: 21

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0227G21"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC2M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 [gil4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
 |||||  
 Db 18 TTAGGG 13

## RESULT 12

TA158A03P/c  
 LOCUS TA158A03P 20 bp DNA linear GSS 13-DEC-2000  
 DEFINITION T. brucei sheared genomic DNA clone 158A03, forward sequence,  
 genomic survey sequence.

ACCESSION AL472050  
 VERSION AL472050.1 GI:11837404

KEYWORDS GSS.

SOURCE Trypanosoma brucei  
 Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

REFERENCE 1 (bases 1 to 20)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (  
 4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.

## FEATURES

source

1..20  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="158A03"

## ORIGIN

Query Match 100.0%; Score 6; DB 29; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
 |||||  
 Db 19 TTAGGG 14

## RESULT 13

TA199G02Q/c  
 LOCUS TA199G02Q 20 bp DNA linear GSS 13-DEC-2000  
 DEFINITION T. brucei sheared genomic DNA clone 199g02, reverse sequence,  
 genomic survey sequence.

ACCESSION AL476798  
 VERSION AL476798.1 GI:11843362

KEYWORDS GSS.

SOURCE Trypanosoma brucei  
 Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

REFERENCE 1 (bases 1 to 20)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (  
 4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.

## FEATURES

source

1..20  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
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## ORIGIN

Query Match 100.0%; Score 6; DB 29; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
 |||||  
 Db 20 TTAGGG 15

## RESULT 14

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 LOCUS AW248826 21 bp mRNA linear EST 07-JAN-2000  
 DEFINITION 2821056.3prime NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:2821056 3',  
 mRNA sequence.

ACCESSION AW248826  
 VERSION AW248826.1 GI:6591819

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 21)

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Other ESTs: 2821056.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

**Tissue Procurement:** DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross\_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 21 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 21 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
 Plate: LLCMS5 row: N column: 1  
 High quality sequence stop: 21.  
 Location/Qualifiers  
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 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

**ORIGIN**

Query Match 100.0%; Score 6; DB 10; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
 |||||  
 Db 20 TTAGGG 15

**RESULT 15**  
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**LOCUS** 2821108.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821108 3',  
**DEFINITION** mRNA sequence.  
**ACCESSION** AW248836  
**VERSION** AW248836.1 GI:6591829  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 21)  
**REFERENCE** NIH-MGC <http://mgc.nci.nih.gov/>.  
**AUTHORS** National Institutes of Health, Mammalian Gene Collection (MGC)  
**TITLE** Unpublished (1999)  
**JOURNAL** Other ESTs: 2821108.5prime  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

**Tissue Procurement:** DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross\_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 10 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 21 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
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 High quality sequence stop: 10.  
 Location/Qualifiers  
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 /clone="IMAGE:2821108"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

# FEATURES

source

1. .21

Location/Qualifiers

/organism="Homo sapiens"

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/clone="IMAGE:2821108"

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/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 7"

/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

# ORIGIN

Query Match 100.0%; Score 6; DB 10; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
 |||||  
 Db 20 TTAGGG 15

Search completed: August 11, 2004, 18:58:54  
 Job time : 723.925 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:38:14 ; Search time 1269.68 Seconds  
(without alignments)  
682.741 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcattacatgacg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rod:\*

36: em\_htg\_nam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	20	100.0	20	6	AX268760	AX268760 Sequence
C 2	14.8	74.0	120	6	E08557	E08557 Synthetic D
C 3	14.8	74.0	120	6	E08566	E08566 Synthetic D
C 4	14.2	71.0	153	6	BD246071	BD246071 Developme
C 5	14.2	71.0	166	11	AF025868	AF025868 Aegilops
C 6	14.2	71.0	178	1	BA1RRDA01	W79375 Bacterium A
C 7	13.8	69.0	162	6	AR355576	AX355576 Sequence
C 8	13.8	69.0	196	6	AX909486	AX909486 Sequence
C 9	13.8	69.0	196	6	BD045019	BD045019 Sequence
C 10	13.6	68.0	58	6	I13500	I13500 Sequence 34
C 11	13.6	68.0	58	6	I13501	I13501 Sequence 35
C 12	13.6	68.0	76	6	E08558	E08558 Synthetic D
C 13	13.6	68.0	76	6	E08558	E08558 Synthetic D
C 14	13.6	68.0	76	6	E08567	E08567 Synthetic D
C 15	13.6	68.0	76	6	E08567	E08567 Synthetic D
C 16	13.6	68.0	135	11	AU049687	AU049687 Rattus o
C 17	13.4	67.0	28	6	E06768	E06768 Synthetic o
C 18	13.4	67.0	28	6	I12026	I12026 Sequence 10
C 19	13.4	67.0	42	6	AR032363	AR032363 Sequence
C 20	13.4	67.0	42	6	I30220	I30220 Sequence 6
C 21	13.4	67.0	70	6	AR032364	AR032364 Sequence
C 22	13.4	67.0	70	6	AR032365	AR032365 Sequence
C 23	13.4	67.0	70	6	I30221	I30221 Sequence 7
C 24	13.4	67.0	70	6	I30221	I30221 Sequence 8
C 25	13.4	67.0	124	6	E08556	E08556 Synthetic D
C 26	13.4	67.0	124	6	E08565	E08565 Synthetic D
C 27	13.2	66.0	33	6	AR285607	AR285607 Sequence
C 28	13.2	66.0	33	6	AX297790	AX297790 Sequence
C 29	13.2	66.0	97	11	AU025275	AU025275 Rattus no
C 30	13.2	66.0	117	4	SHPMAF36P	M80519 Ovis aries
C 31	13.2	66.0	134	8	AX594611	AX594611 Arabidops
C 32	13.2	66.0	152	6	AX912126	AX912126 Sequence
C 33	13.2	66.0	152	6	BD047659	BD047659 Sequence
C 34	13.2	66.0	177	6	AR244933	AR244933 Sequence
C 35	13.2	66.0	187	11	G03687	G03687 human STS W
C 36	13.2	66.0	194	11	BX546013	BX546013 Arabidops
C 37	13	65.0	17	6	AX194495	AX194495 Sequence
C 38	13	65.0	17	6	AX465445	AX465445 Sequence
C 39	13	65.0	33	6	AX684461	AX684461 Sequence
C 40	13	65.0	133	9	HUMPODAT07	D17705 Homo sapien
C 41	13	65.0	150	6	AX196369	AX196369 Sequence
C 42	13	65.0	150	6	AX196371	AX196371 Sequence
C 43	13	65.0	180	8	CNS01D6K	AL116436 Botrytis
C 44	12.8	64.0	91	10	MMSCFT3	AF083887 Mus muscu
C 45	12.8	64.0	102	11	BX663678	BX663678 Arabidops

ALIGNMENTS

RESULT 1  
AX268760  
LOCUS AX268760 20 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 8 from Patent WO0174342.  
ACCESSION AX268760  
VERSION AX268760.1 GI:16541832  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS 1  
TITLE Gilchrist,B.A., Yaar,M. and Eller,M.  
JOURNAL Use of locally applied dna fragments  
Patent: WO 0174342-A 8 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)

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FEATURES
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
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  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTACGTACG 20
Db 1 GCATGCATGCATTACGTACG 20

RESULT 2
E08557/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
  OS None
  OC Artificial sequences.
  PN JP 1994343498-A/3
  PD 20-DEC-1994
  PF 03-JUN-1993 JP 1993133640
  PI KATO KINYA, KURIYAMA AKIRA
  PC C12Q1/68;
  CC strandedness: Single;
  CC topology: Linear;
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QY 1 GCATGCATGCATTACGTA 18
Db 24 GCATGCATGCATTATATA 7

RESULT 4
BD246071/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
  OS Staphylococcus aureus bacteriophage 44AHJD
  PN JP 2002531107-A/806
  PD 24-SEP-2002
  PF 03-DEC-1999 JP 2000585456
  PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
  28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
  01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
  PELLETIER,PHILLIPE GROS,MICHAEL DUBOW
  PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
  PC C12M1/00,
  PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
  C12N15/00,
  PC A61K37/02
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TITLE
JOURNAL
COMMENT
  METHOD FOR DETECTING NUCLEIC ACID
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  OC Artificial sequences.
  PN JP 1994343499-A/4
  PD 20-DEC-1994
  PF 04-JUN-1993 JP 1993134615
  PI KATO KINYA
  PC C12Q1/68;
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  CC topology: Linear;
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      /db_xref="taxon:32644"
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  Best Local Similarity 88.9%; Score 14.8; DB 6; Length 120;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTACGTA 18
Db 24 GCATGCATGCATTATATA 7

RESULT 4
BD246071/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
  OS Staphylococcus aureus bacteriophage 44AHJD
  PN JP 2002531107-A/806
  PD 24-SEP-2002
  PF 03-DEC-1999 JP 2000585456
  PR 03-DEC-1998 US 60/110992,03-JUN-1999 US 09/326144 PR
  28-SEP-1999 US 09/407804,30-SEP-1999 US 60/157218 PR
  01-DEC-1999 US 60/168777,02-DEC-1999 US 09/454252 PI JERRY
  PELLETIER,PHILLIPE GROS,MICHAEL DUBOW
  PC C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
  PC C12M1/00,
  PC C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
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  PC A61K37/02
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Query Match      71.0%; Score 14.2; DB 6; Length 153;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19
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DB 70 GCATACCTGCATTACGTTTC 52

RESULT 5
AF025868          166 bp DNA linear STS 12-JAN-2001
LOCUS             Aegilops markgrafii RAPD marker generated by Operon primer OP003,
DEFINITION        sequence tagged site.
ACCESSION          AF025868
VERSION            AF025868.1 GI:4090919
KEYWORDS           STS.
SOURCE             Aegilops markgrafii
ORGANISM           Aegilops markgrafii
REFERENCE          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE              Poideae; Triticeae; Aegilops.
REFERENCE          1 (bases 1 to 166)
AUTHORS            Sun, L.-H. and Wang, R.R.-C.
TITLE              Identification and sequences of RAPD markers for Aegilops caudata
                  chromosomes
JOURNAL            Unpublished
REFERENCE          2 (bases 1 to 166)
AUTHORS            Sun, L.-H. and Wang, R.R.-C.
TITLE              Direct Submission
JOURNAL            Submitted (20-SEP-1997) FRRL, USDA-ARS, 695 N 1100 E, Logan, UT
                  84322-6300, USA
FEATURES           Location/Qualifiers
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                    /chromosome="F; G"
                    /note="RAPD marker generated by Operon primer OP003; C
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                    amphiploid of Triticum aestivum X Aegilops caudata"
primer_bind       1..10
                  /PCR_conditions="25 ul reaction mix containing 1X buffer,
                  3 mM MgCl2, 2 units of AmpliTaq DNA polymerase Stoffel
                  fragment (Perkin Elmer), 0.24 mM dNTP, 100 ng primer, and
                  40 ng template DNA. Amplification was accomplished with 40
                  cycles of 1 min at 94 C, 1 min at 36 C, and 2 min at 72 C
                  using the fastest transitions available"
primer_bind       complement(156..166)

ORIGIN
Query Match      71.0%; Score 14.2; DB 11; Length 166;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTACG 20
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DB 48 CATGCAAGATTACTTACG 66

RESULT 6
BAIRDA01/c        178 bp rRNA linear BCT 26-JAN-1996
LOCUS             Bacterium ALV 16S rRNA sequence.
DEFINITION        M79375
ACCESSION          M79375.1 GI:173814
KEYWORDS           16S ribosomal RNA.
SEGMENT           1 of 3
SOURCE            bacterium ALV
ORGANISM           Bacterium ALV
REFERENCE          1 (bases 1 to 178)
AUTHORS            Lane, D.J., Harrison, A.P. Jr., Stahl, D., Pace, B., Giovannoni, S.J.,

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Olsen, G.J. and Pace, N.R.
Evolutionary relationships among sulfur- and iron-oxidizing
subacteria
J. Bacteriol. 174 (1), 269-278 (1992)
MEDLINE 92104973
PUBMED 1729214
COMMENT Original source text: Bacterium ALV (individual isolate ALV) rRNA.
FEATURES           Location/Qualifiers
                    1..178
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Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTACG 20
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DB 60 CTTGCAATGATTACGCACG 42

RESULT 7
AR355576          162 bp DNA linear PAT 17-AUG-2003
LOCUS             Sequence 1694 from patent US 6593114.
DEFINITION        AR355576
ACCESSION          AR355576
VERSION            AR355576.1 GI:33761660
KEYWORDS           .
SOURCE            Unknown.
ORGANISM           Unclassified.
REFERENCE          1 (bases 1 to 162)
AUTHORS            Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
                  Rosen, C.A.
TITLE              Staphylococcus aureus polynucleotides and sequences
JOURNAL            Patent: US 6593114-A 1694 15-JUL-2003;
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Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCATGCATTACGTACG 20
    ||||| ||||| ||||| |||||
DB 50 TACATGCAATACGTACG 66

RESULT 8
AX909486/c        196 bp DNA linear PAT 18-DEC-2003
LOCUS             Sequence 25349 from Patent EP1033401.
DEFINITION        AX909486
ACCESSION          AX909486
VERSION            AX909486.1 GI:40065566
KEYWORDS           .
SOURCE            Homo sapiens (human)
ORGANISM           Homo sapiens
REFERENCE          1
AUTHORS            Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE              Expressed sequence tags and encoded human proteins
JOURNAL            Patent: EP 1033401-A 25349 06-SEP-2000;
                  Genset (FR)

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  Query Match      69.0%; Score 13.8; DB 6; Length 196;
  Best Local Similarity 88.2%; Pred. No. 1.9e+04;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY  3 ATGCATGCATTACGTAC 19
    ||||| ||| |||
DB   31 ATGCATGCTTTATGTAC 15

RESULT 9
BD045019/c
LOCUS      BD045019          196 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION  BD045019
VERSION    BD045019.1 GI:22586761
KEYWORDS  JP 2001269182-A/21265.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLES    Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
JOURNAL   Sequence tag and encoded human protein
          Patent: JP 2001269182-A 21265 02-OCT-2001;
          GENSET
COMMENT   OS Homo sapiens (human)
          PN JP 2001269182-A/21265
          PD 02-OCT-2001
          PF 24-FEB-2000 JP 2000118773
          PR 26-FEB-1999 US 60/122487
          PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
          PI JORDAN
          PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
          PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
          CC G06F15/40
          FH Key
          Location/Qualifiers
          1..196
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
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  source
    Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
ORIGIN
  Query Match      69.0%; Score 13.8; DB 6; Length 196;
  Best Local Similarity 88.2%; Pred. No. 1.9e+04;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY  3 ATGCATGCATTACGTAC 19
    ||||| ||| |||
DB   31 ATGCATGCTTTATGTAC 15

RESULT 10
I13500
LOCUS      I13500          58 bp      DNA      linear      PAT 26-JUL-1995
DEFINITION Sequence 34 from patent US 5436391.
ACCESSION  I13500
VERSION    I13500.1 GI:910841
KEYWORDS
SOURCE
ORGANISM  Unknown.
REFERENCE  1 (bases 1 to 58)
AUTHORS   Fujimoto, H., Ito, K., Yamamoto, M. and Shimamoto, K.
TITLE     Synthetic insecticidal gene, plants of the genus oryza transformed
JOURNAL   with the gene, and production thereof
          Patent: US 5436391-A 34 25-JUL-1995;
          Location/Qualifiers
          1..58
          /organism="unknown"
          /mol_type="unassigned DNA"
ORIGIN
  Query Match      68.0%; Score 13.6; DB 6; Length 58;
  Best Local Similarity 80.0%; Pred. No. 2.7e+04;
  Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY  1 GCATGCATGCATTACGTACG 20
    ||||| ||| |||
DB   9 GCATGCATGAATTCCTAGG 28

RESULT 11
I13501/c
LOCUS      I13501          58 bp      DNA      linear      PAT 26-JUL-1995
DEFINITION Sequence 35 from patent US 5436391.
ACCESSION  I13501
VERSION    I13501.1 GI:910842
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 58)
AUTHORS   Fujimoto, H., Ito, K., Yamamoto, M. and Shimamoto, K.
TITLE     Synthetic insecticidal gene, plants of the genus oryza transformed
JOURNAL   with the gene, and production thereof
          Patent: US 5436391-A 35 25-JUL-1995;
          Location/Qualifiers
          1..58
          /organism="unknown"
          /mol_type="unassigned DNA"
ORIGIN
  Query Match      68.0%; Score 13.6; DB 6; Length 58;
  Best Local Similarity 80.0%; Pred. No. 2.7e+04;
  Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY  1 GCATGCATGCATTACGTACG 20
    ||||| ||| |||
DB   54 GCATGCATGAATTCCTAGG 35

RESULT 12
E08558
LOCUS      E08558          76 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Synthetic DNA for probes and primers.
ACCESSION  E08558
VERSION    E08558.1 GI:2176673
KEYWORDS  JP 1994343498-A/4.
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE  1 (bases 1 to 76)
AUTHORS   Kato, K. and Kuriyama, A.
TITLE     NUCLEIC ACID PROBE AND METHOD FOR DETECTING NUCLEIC ACID
JOURNAL   Patent: JP 1994343498-A 4 20-DEC-1994;
          CANON INC
COMMENT   OS None
          OC Artificial sequences.
          PN JP 1994343498-A/4
          PD 20-DEC-1994
          PF 03-JUN-1993 JP 1993133640
          PI KATO KINYA, KURIYAMA AKIRA
          PC C12Q1/68;
          CC strandedness: Single;
          CC topology: Linear;
          FH Key
          Location/Qualifiers

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FH      source
FT      1. .76
FT      /organism='Artificial sequences'.
FEATURES
source
  Location/Qualifiers
    1. .76
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    /db_xref="taxon:32644"
ORIGIN
Query Match      68.0%; Score 13.6; DB 6; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      1 GCATGCATGCATTACGTACG 20
      |||||
Db      53 GCATGCATGCATCGCGCGG 72
      |||||

RESULT 13
E08558/c
LOCUS      E08558      76 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Synthetic DNA for probes and primers.
ACCESSION E08558
VERSION   E08558.1 GI:2176673
KEYWORDS JP 1994343498-A/4.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 76)
AUTHORS   Kato,K. and Kuriyama,A.
TITLE     NUCLEIC ACID PROBE AND METHOD FOR DETECTING NUCLEIC ACID
JOURNAL   Patent: JP 1994343498-A 4 20-DEC-1994;
          CANON INC
COMMENT   OS None
          OC Artificial sequences.
          PN JP 1994343498-A/4
          PD 20-DEC-1994
          PF 03-JUN-1993 JP 1993133640
          PI KATO KINYA, KURIYAMA AKIRA
          PC C12Q1/68;
          CC strandedness: Single;
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FEATURES
source
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
ORIGIN
Query Match      68.0%; Score 13.6; DB 6; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      1 GCATGCATGCATTACGTACG 20
      |||||
Db      26 GCATGCATGCATCGCTCG 7
      |||||

RESULT 14
E08567/c
LOCUS      E08567      76 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Synthetic DNA for probe and primer.
ACCESSION E08567
VERSION   E08567.1 GI:2176682
KEYWORDS JP 1994343499-A/5.
SOURCE    unidentified
ORGANISM  unclassified.

```

```

REFERENCE 1 (bases 1 to 76)
AUTHORS   Kato,K.
TITLE     METHOD FOR DETECTING NUCLEIC ACID
JOURNAL   Patent: JP 1994343499-A 5 20-DEC-1994;
          CANON INC
COMMENT   OS None
          OC Artificial sequences.
          PN JP 1994343499-A/5
          PD 20-DEC-1994
          PF 04-JUN-1993 JP 1993134615
          PI KATO KINYA
          PC C12Q1/68;
          CC strandedness: Single;
          CC topology: Linear;
          FH Key
          FT source
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          FT      /organism='Artificial sequences'.
FEATURES
source
  Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
ORIGIN
Query Match      68.0%; Score 13.6; DB 6; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      1 GCATGCATGCATTACGTACG 20
      |||||
Db      53 GCATGCATGCATCGCGCGG 72
      |||||

RESULT 15
E08567/c
LOCUS      E08567      76 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Synthetic DNA for probe and primer.
ACCESSION E08567
VERSION   E08567.1 GI:2176682
KEYWORDS JP 1994343499-A/5.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 76)
AUTHORS   Kato,K.
TITLE     METHOD FOR DETECTING NUCLEIC ACID
JOURNAL   Patent: JP 1994343499-A 5 20-DEC-1994;
          CANON INC
COMMENT   OS None
          OC Artificial sequences.
          PN JP 1994343499-A/5
          PD 20-DEC-1994
          PF 04-JUN-1993 JP 1993134615
          PI KATO KINYA
          PC C12Q1/68;
          CC strandedness: Single;
          CC topology: Linear;
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FEATURES
source
  Location/Qualifiers
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    /db_xref="taxon:32644"
ORIGIN
Query Match      68.0%; Score 13.6; DB 6; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      1 GCATGCATGCATTACGTACG 20
      |||||
Db      53 GCATGCATGCATCGCGCGG 72
      |||||

RESULT 16
E08567/c
LOCUS      E08567      76 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Synthetic DNA for probe and primer.
ACCESSION E08567
VERSION   E08567.1 GI:2176682
KEYWORDS JP 1994343499-A/5.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 76)
AUTHORS   Kato,K.
TITLE     METHOD FOR DETECTING NUCLEIC ACID
JOURNAL   Patent: JP 1994343499-A 5 20-DEC-1994;
          CANON INC
COMMENT   OS None
          OC Artificial sequences.
          PN JP 1994343499-A/5
          PD 20-DEC-1994
          PF 04-JUN-1993 JP 1993134615
          PI KATO KINYA
          PC C12Q1/68;
          CC strandedness: Single;
          CC topology: Linear;
          FH Key
          FT source
          FT      1. .76
          FT      /organism='Artificial sequences'.
FEATURES
source
  Location/Qualifiers
    1. .76
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
ORIGIN
Query Match      68.0%; Score 13.6; DB 6; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      1 GCATGCATGCATTACGTACG 20
      |||||
Db      26 GCATGCATGCATCGCTCG 7
      |||||

RESULT 17
E08567/c
LOCUS      E08567      76 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Synthetic DNA for probe and primer.
ACCESSION E08567
VERSION   E08567.1 GI:2176682
KEYWORDS JP 1994343499-A/5.
SOURCE    unidentified
ORGANISM  unclassified.

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OY 1 GCATGCATGCATTACGTACG 20  
|||  
Db 26 GCATGCATGCATCACGCTCG 7  
|||

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Job time : 1272.68 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 15:32:08 ; Search time 289.032 Seconds  
(without alignments)  
293.960 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcattacattacg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3774412

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002s.\*  
7: geneseqn2003as.\*  
8: geneseqn2003bs.\*  
9: geneseqn2003cs.\*  
10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20	100.0	20	2	Aaz10697 Oligonucl
2	20	100.0	20	4	Aas14912 Melanogen
3	20	100.0	20	8	ACD25827 Melanogen
4	20	100.0	20	8	ACD25777 Oligonucl
5	15.2	76.0	42	6	ABK91410 Multiple
6	15.2	76.0	42	6	ABK91409 Multiple
7	14.8	74.0	120	2	AAQ95093 Configur
8	14.8	74.0	120	2	AAQ84038 Plasmid p
9	14.2	71.0	141	7	ACA23973 Prokaryot
10	14.2	71.0	153	3	AAAG9048 Bacteriop
11	13.8	69.0	162	2	AAV76005 Staphyloc
12	13.8	69.0	196	3	AAAC21274 Human sec
13	13.6	68.0	28	2	AAT29051 Maltogen
14	13.6	68.0	76	2	AAQ95094 Configur
15	13.6	68.0	76	2	AAQ95094 Configur
16	13.6	68.0	76	2	AAQ84039 Plasmid p
17	13.6	68.0	76	2	AAQ84039 Plasmid p
18	13.4	67.0	70	2	AAQ35972 Oligonucl
19	13.4	67.0	124	2	AAQ95092 Configur
20	13.4	67.0	124	2	AAQ84037 Plasmid p
21	13.4	67.0	175	7	ABX91312 Murine ge
22	13.2	66.0	33	5	AAAD19573 Rhizopus
23	13.2	66.0	152	3	AAAC23914 Human sec

C 24	13.2	66.0	177	7	ABX81832 Corn ear-
C 25	13	65.0	17	4	AAC80675 Immunogen
C 26	13	65.0	17	4	AAS09645 Immunorea
C 27	13	65.0	17	6	ABK46523 Immunosti
C 28	13	65.0	33	7	AAD48011 BGMV DNAB
C 29	13	65.0	130	6	ABL75969 Corn tass
C 30	13	65.0	150	5	AAI61445 Soybean 2
C 31	13	65.0	150	5	AAI61447 Soybean 2
C 32	12.8	64.0	37	7	ABZ69169 E coli is
C 33	12.8	64.0	40	2	AAT34008 Primer fo
C 34	12.8	64.0	60	6	ABN37518 Human spl
C 35	12.8	64.0	99	2	AAQ34156 Downstrea
C 36	12.8	64.0	138	3	AAC59405 Human sec
C 37	12.8	64.0	182	3	AAC08211 Human sec
C 38	12.8	64.0	195	7	ACF56778 Rice endo
C 39	12.6	63.0	26	2	AAQ46972 Helper Pr
C 40	12.6	63.0	27	3	AAA15194 PCR prime
C 41	12.6	63.0	32	3	AAA37803 Helicobac
C 42	12.6	63.0	33	6	ABA04987 Human tel
C 43	12.6	63.0	41	6	ABV76426 Ribosomal
C 44	12.6	63.0	59	9	ADB39029 Sample DN
C 45	12.6	63.0	65	3	AAA14518 PCR prime

## ALIGNMENTS

RESULT 1  
AAZ10697  
ID AAZ10697 standard; DNA; 20 BP.  
XX  
AC AAZ10697;  
XX  
DT 23-NOV-1999 (first entry)  
XX  
DE Oligonucleotide sequence that increases p53 activity in a cell.  
XX  
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
KW skin cancer; ss.  
XX  
OS Synthetic.  
XX  
FN GB2336157-A.  
XX  
PD 13-OCT-1999.  
XX  
PF 24-MAR-1999; 99GB-00006758.  
XX  
PR 26-MAR-1998; 98US-00048927.  
XX  
PA (UYBO-) UNIV BOSTON.  
XX  
PI Gilchrist BA, Yaar M, Eller M;  
XX  
DR WPI; 1999-543520/46.  
XX  
PT DNA fragments useful for increasing p53 activity in a cell and reducing  
PT susceptibility to UV-induced hyperproliferative diseases.  
XX  
PS Claim 11; Page 30; 44pp; English.  
XX  
CC AAZ10692-97 represent DNA fragments that are used for increasing p53  
CC activity in a cell. The oligonucleotides are UV mimetics and protect  
CC cells against subsequent exposure to UV-irradiation or chemicals. The  
CC oligonucleotides are useful for increasing p53 activity in a cell.  
CC reducing the susceptibility to UV-induced hyperproliferative diseases,  
CC treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,  
CC conjunctivitis, and UV-induced dermatoses, reducing photoaging and  
XX reducing susceptibility to skin cancer  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20  
DB 1 GCATGCATGCATTACGTACG 20

RESULT 2  
ID AAS14912 standard; DNA; 20 BP.  
XX AAS14912;  
DT 14-FEB-2002 (first entry)  
XX Melanogenesis associated oligonucleotide #8.

DE Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
XX Synthetic.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= g  
FT /note= "Phosphorylated"

WO200174342-A2.  
XX  
PD 11-OCT-2001.  
XX  
XX  
PF 30-MAR-2001; 2001WO-US010162.  
XX  
XX 31-MAR-2000; 2000US-00540843.  
XX (UYBO-) UNIV BOSTON.  
PA Gilchrest BA, Yaar M, Eller M;  
XX  
PI Gilchrest BA, Yaar M, Eller M;  
XX  
DR WPI; 2001-626338/72.  
XX

Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light.

Claim 1; Page 39; 74pp; English.

The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to

CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
CC oligonucleotides that contain non-hydrolyzable backbones are used to  
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
CC sequence is melanogenesis associated oligonucleotide #8, a synthetic  
CC peptide that resembles the fragment excised during excision repair of  
CC thymine dimers and one of the oligonucleotides used to inhibit mammalian  
CC epithelial cell proliferation, described in the method of the invention  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20  
DB 1 GCATGCATGCATTACGTACG 20

RESULT 3  
ID ACD25827 standard; DNA; 20 BP.  
XX ACD25827;  
AC ACD25827;  
DT 08-SEP-2003 (first entry)  
XX  
XX Melanogenic telomere-like oligonucleotide #2.

DE Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological;  
KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;  
KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;  
KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;  
KW gp-1100; hyperproliferative disorder; spongiosis; blistering;  
KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;  
KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;  
KW atopic dermatitis; breast cancer; lung cancer; liver cancer;  
KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;  
KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;  
KW stomach cancer; thyroid cancer.  
XX Synthetic.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5' phosphorylated"

US2003032610-A1.  
XX  
PD 13-FEB-2003.  
XX  
XX 12-APR-2002; 2002US-00122630.  
XX  
XX 03-JUN-1996; 96WO-US008386.  
PR 26-MAR-1998; 98US-00048927.  
PR 31-MAR-2000; 2000US-00540843.  
PR 30-MAR-2001; 2001WO-US010162.  
XX (GILC/) GILCHREST B A.  
PA (ELLE/) ELLER M S.  
PA (YAAR/) YAAR M.  
XX  
PI Gilchrest BA, Eller MS, Yaar M;  
XX  
DR WPI; 2003-512221/48.  
XX

Inhibiting growth of cancer cells and inducing apoptosis in cancer cells, by administering composition having oligonucleotides that share sequence identity with human telomere overhang repeat.

Claim 44; Page 18; 65pp; English.

XX The invention relates to inhibiting growth of cancer cells, which is  
 CC independent of presence or activity of telomerase in cells, not requiring  
 CC the presence or activity of p53 normal function in cells, or resulting in  
 CC S-phase arrest in cells, and inducing apoptosis in cancer cells,  
 CC involving administering a composition comprising oligonucleotides which  
 CC share at least 50% sequence identity with human telomere overhang repeat,  
 CC (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their  
 CC contiguous portion) and is used in a method inhibiting proliferation of  
 CC epithelial cells in a mammal or preventing/reducing DNA damage in cells  
 CC of a mammal, where the DNA damage is caused by radiation or DNA-damaging  
 CC chemicals. The method is useful for inhibiting growth of cancer cells  
 CC (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,  
 CC squamous cell carcinoma), for inducing apoptosis in cancer cells in  
 CC human, promoting differentiation of malignant cells in a mammal,  
 CC enhancing the expression of one or more surface antigens (e.g. MART-1,  
 CC tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer  
 CC cells (especially melanoma cells) in a human and for treatment of other  
 CC hyperproliferative disorders (e.g. spongiolysis, blistering or dyskeratosis  
 CC in the skin of a mammal, skin cancer in a human with xeroderma  
 CC pigmentosum, seboreic keratosis, actinic keratosis, Bowen's disease, or  
 CC basal cell carcinoma) and for treating or preventing pre-cancerous  
 CC conditions affecting epithelial cells (such as psoriasis and atopic  
 CC dermatitis) and also the types of cancers of breast, lung, liver,  
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,  
 CC oesophagus, stomach, and thyroid. The present sequence is a melanogenic  
 CC telomere-like oligonucleotide of the invention  
 XX  
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCATGCATGCATTACGTACG 20  
 Db 1 GCATGCATGCATTACGTACG 20  
 RESULT 4  
 ACD25777  
 ID ACD25777 standard; DNA; 20 BP.  
 XX ACD25777;  
 AC ACD25777;  
 XX  
 DT 28-AUG-2003 (first entry)  
 XX  
 DE Oligonucleotide with homology to telomere pTPT sequence.  
 KW ss; human telomere overhang repeat; proliferative disease; cytostatic;  
 KW antiproliferative; dermatological; cancer; apoptosis; skin cancer;  
 KW UV irradiation-induced skin; oxidative damage; lymphoma; osteosarcoma;  
 KW melanoma; leukaemia; cervical cancer; squamous cell carcinoma;  
 KW spongiolysis; blistering; dyskeratosis; xeroderma pigmentosum;  
 KW seboreic keratosis; actinic keratosis; Bowen's disease;  
 KW basal cell carcinoma; pre-cancerous condition; epithelial cell;  
 KW psoriasis; atopic dermatitis.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /tag= a  
 FT /mod base= OTHER  
 FT /note= "5, phosphorylated"  
 XX  
 PN US2003032611-A1.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 12-APR-2002; 2002US-00122633.  
 XX  
 PF 31-MAR-2000; 2000US-00540843.  
 PR

PR 30-MAR-2001; 2001WO-US010162.  
 XX (GILC/) GILCREST B A.  
 PA (ELLE/) ELLER M S.  
 PA (YAAR/) YAAR M.  
 XX  
 PI Gilcrest BA, Eller MS, Yaar M;  
 XX  
 DR WPI; 2003-512222/48.  
 XX  
 PT Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,  
 PT by administering composition having oligonucleotides that share sequence  
 PT identity with human telomere overhang repeat.  
 XX  
 PS Claim 44; Page 18; 64pp; English.  
 XX  
 CC The invention relates to inhibiting growth of cancer cells (which is  
 CC independent of the presence or activity of telomerase in cells) not  
 CC requiring the presence or activity of p53 normal function in cells, or  
 CC resulting in S-phase arrest in cells, and inducing apoptosis in the  
 CC cancer cells, comprising administering a composition comprising  
 CC oligonucleotides which share at least 50% sequence identity with human  
 CC telomere overhang repeat (TTAGG)n. The method also involves promoting  
 CC differentiation of malignant cells in a mammal, enhancing the expression  
 CC of one or more surface antigens indicative of differentiation of cancer  
 CC cells in a human, by administering the oligonucleotide. The  
 CC oligonucleotide is further administered to enhance repair of UV  
 CC irradiation-induced damage to the skin in a human, reduce oxidative  
 CC damage in a mammal and to reduce proliferation of keratinocytes in the  
 CC skin of a human. The composition comprises oligonucleotides such as  
 CC pGAGTATGAG, pCATAC, pGTAGGTTAG, pGGTATGGTT, pTAGATGGTG, and a  
 CC physiological carrier. Oligonucleotides such as pTAGAGGAT, pAGTATGA,  
 CC pGTATG, pCCCTAA, pAGTATGA and pGCATGCATGCATTACGTACG may be administered  
 CC along with those detailed above. The method is useful for inhibiting  
 CC growth of cancer cells, especially lymphoma, osteosarcoma, melanoma,  
 CC leukaemia, cervical cancer, squamous cell carcinoma, in a human. The  
 CC method is also useful for inducing apoptosis in cancer cells in human,  
 CC promoting differentiation of malignant cells in a mammal and enhancing  
 CC the expression of one or more surface antigens (e.g. MART-1, tyrosinase,  
 CC TRP-1 or gp-1100) indicative of differentiation of cancer cells,  
 CC especially melanoma cells, for inhibiting proliferation of epithelial  
 CC cells, for preventing or reducing DNA damage in epithelial cells in a  
 CC mammal, where the cells are epithelial cells. The composition is  
 CC preferably useful for treating a hyperproliferative disorder in human. A  
 CC composition comprising pGAGTATGAG and pTPT, is useful for preventing  
 CC spongiolysis, blistering or dyskeratosis in the skin of a mammal, following  
 CC exposure to UV light, reducing the occurrence of skin cancer in a human  
 CC with xeroderma pigmentosum or for enhancing repair of UV irradiation-  
 CC induced damage to skin in a human, treating melanoma and reducing  
 CC proliferation of keratinocytes in the skin, where the human has  
 CC seboreic keratosis, actinic keratosis, Bowen's disease, squamous cell  
 CC carcinoma or basal cell carcinoma. The method is useful for treating or  
 CC preventing pre-cancerous conditions affecting epithelial cells such as  
 CC psoriasis and atopic dermatitis, and also the types of cancers of breast,  
 CC lung, liver, prostate, pancreatic, ovarian, bladder, uterine, colon,  
 CC brain, oesophagus, stomach, and thyroid. The present sequence is a  
 CC oligonucleotide with homology to the telomere pTPT sequence shown to  
 CC increase pigmentation in melanoma cells  
 XX  
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCATGCATGCATTACGTACG 20  
 Db 1 GCATGCATGCATTACGTACG 20  
 RESULT 5  
 ABK91410  
 ID ABK91410 standard; DNA; 42 BP.

```

XX AC ABK91410;
XX DT 05-NOV-2002 (first entry)
XX DE Multiple cloning site for retroviral vectors #2.
XX ds; long terminal repeat; LTR; gag; cytostatic; multiple cloning site;
KW envelope protein; retroviral vector; cancer; virally-induced disease;
KW virucide; gene therapy.
XX OS Synthetic.
XX PN WO200260490-A1.
XX PD 08-AUG-2002.
XX PF 31-JAN-2002; 2002WO-US002632.
XX PR 31-JAN-2001; 2001US-0265123P.
XX PA (UYDU-) UNIV DUKE.
XX PI Smith CA, Gilboa E;
XX DR WPI; 2002-619210/66.
XX PT A new Moloney Murine Leukemia Virus-based retroviral vector, designated
PT as LUV, useful for expressing a retroviral cell for treating genetic
PT disorders, or diseases induced by pathogens such as cancer or virally-
PT induced disease.
XX Example 1; Page 13; 50pp; English.
XX The invention relates to a retroviral vector comprising 5' to 3' and in
CC operable linkage, a 5' long terminal repeat (LTR), a splice donor, a
CC packaging sequence, a gag open reading frame (ORF) mutated to reduce
CC translation of gag peptides, a splice acceptor, a start codon in frame
CC with a DNA sequence and a 3' LTR. Also included are producing an
CC infectious viral particle comprising transfecting the retroviral vector
CC into a retroviral packaging cell line under conditions to produce the
CC viral particle, and recovering the viral particle, a packaging cell
CC comprising the retroviral vector, introducing a transcription unit into a
CC eukaryotic cell comprising the retroviral vector or the viral particle or
CC a pharmaceutical composition comprising the retroviral vector, a
CC packaging cell infected by the viral particle, and a carrier, diluent,
CC as cancer or virally induced disease. The methods are useful for
CC cell for treating genetic disorders or diseases induced by pathogens such
CC as cancer or virally induced disease. The methods are useful for
CC preparing the retroviral vector. The vector provides high titre,
CC efficient expression of foreign genes, and safety. The present sequence
CC is a multiple cloning site suitable for inclusion in the vectors of the
CC invention
XX SQ Sequence 42 BP; 8 A; 13 C; 15 G; 6 T; 0 U; 0 Other;
XX Query Match 76.0%; Score 15.2; DB 6; Length 42;
XX Best Local Similarity 85.0%; Pred. No. 3 8e-02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 GCATCGCATGCAATTAGCTAGC 20
XX DB 23 GCGTCGATGCGGCGTAGC 42
XX RESULT 6
XX ABK91409/c
XX ID ABK91409 standard; DNA; 42 BP.
XX AC ABK91409;
XX DT 05-NOV-2002 (first entry)

```

```

XX DE Multiple cloning site for retroviral vectors #1.
XX ds; long terminal repeat; LTR; gag; cytostatic; multiple cloning site;
KW envelope protein; retroviral vector; cancer; virally-induced disease;
KW virucide; gene therapy.
XX OS Synthetic.
XX PN WO200260490-A1.
XX PD 08-AUG-2002.
XX PF 31-JAN-2002; 2002WO-US002632.
XX PR 31-JAN-2001; 2001US-0265123P.
XX PA (UYDU-) UNIV DUKE.
XX PI Smith CA, Gilboa E;
XX DR WPI; 2002-619210/66.
XX PT A new Moloney Murine Leukemia Virus-based retroviral vector, designated
PT as LUV, useful for expressing a retroviral cell for treating genetic
PT disorders, or diseases induced by pathogens such as cancer or virally-
PT induced disease.
XX Example 1; Page 13; 50pp; English.
XX The invention relates to a retroviral vector comprising 5' to 3' and in
CC operable linkage, a 5' long terminal repeat (LTR), a splice donor, a
CC packaging sequence, a gag open reading frame (ORF) mutated to reduce
CC translation of gag peptides, a splice acceptor, a start codon in frame
CC with a DNA sequence and a 3' LTR. Also included are producing an
CC infectious viral particle comprising transfecting the retroviral vector
CC into a retroviral packaging cell line under conditions to produce the
CC viral particle, and recovering the viral particle, a packaging cell
CC comprising the retroviral vector, introducing a transcription unit into a
CC eukaryotic cell comprising the retroviral vector or the viral particle or
CC a pharmaceutical composition comprising the retroviral vector, a
CC packaging cell infected by the viral particle, and a carrier, diluent,
CC as cancer or virally induced disease. The methods are useful for
CC cell for treating genetic disorders or diseases induced by pathogens such
CC as cancer or virally induced disease. The methods are useful for
CC preparing the retroviral vector. The vector provides high titre,
CC efficient expression of foreign genes, and safety. The present sequence
CC is a multiple cloning site suitable for inclusion in the vectors of the
CC invention
XX SQ Sequence 42 BP; 6 A; 15 C; 13 G; 8 T; 0 U; 0 Other;
XX Query Match 76.0%; Score 15.2; DB 6; Length 42;
XX Best Local Similarity 85.0%; Pred. No. 3 8e-02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 GCATCGCATGCAATTAGCTAGC 20
XX DB 24 GCGTCGATGCGGCGTAGC 5
XX RESULT 7
XX AAQ95093/c
XX ID AAQ95093 standard; DNA; 120 BP.
XX AC AAQ95093;
XX DT 02-OCT-1995 (first entry)
XX DE Configuration detecting nucleic acid probe #3.
XX KW Probe; PCR; terminus; amplify; primer; configuration; ss.

```

XX OS Synthetic.

XX FH Key

XX FT primer\_bind Location/Qualifiers

XX FT 1..12 /\*tag= a

XX FT /note= "PCR primer binding site"

XX FT 109..120 /\*tag= b

XX FT /note= "PCR primer binding site"

XX FT

XX PN JP06343498-A.

XX PD 20-DEC-1994.

XX XX

XX XX 03-JUN-1993; 93JP-00133640.

XX PR 03-JUN-1993; 93JP-00133640.

XX PA (CANO ) CANON KK.

XX XX WPI; 1995-069322/10.

XX DR

XX PT Nucleic acid probe - and method for detecting nucleic acid.

XX PS Example 1; Col 4; 6pp; Japanese.

XX CC Probes (AAQ95091-4) can be used in a method for the detection of a

XX CC nucleic acid target sequence which has PCR-controlled termini and can be

XX CC amplified by PCR. The probes can be used to detect configuration

XX SQ Sequence 120 BP; 30 A; 30 C; 30 G; 30 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 2; Length 120;

Best Local Similarity 88.9%; Pred. No. 6.6e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTA 18

Db 24 GCATGCATGCATTATATA 7

RESULT 8

AAQ84038/c

ID AAQ84038 standard; DNA; 120 BP.

XX AC AAQ84038;

XX DT 03-OCT-1995 (first entry)

XX XX Plasmid pCU19 oligonucleotide fragment.

XX XX Plasmid pUC19; oligonucleotide fragment; DNA detection method; ss.

XX OS Synthetic.

XX XX JP06343499-A.

XX PD 20-DEC-1994.

XX XX

XX XX 04-JUN-1993; 93JP-00134615.

XX PR 04-JUN-1993; 93JP-00134615.

XX PA (CANO ) CANON KK.

XX DR WPI; 1995-069323/10.

XX PT Method for detecting nucleic acid - using nucleic acid probe and PCR

XX PT amplification.

XX PS Example 1; Page 4; 9pp; Japanese.

CC AAQ84036-Q84040 are oligonucleotide fragments of the plasmid pUC19, they

CC were used in the construction of the plasmid to demonstrate a new method

CC of DNA detection

XX SQ Sequence 120 BP; 30 A; 30 C; 30 G; 30 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 2; Length 120;

Best Local Similarity 88.9%; Pred. No. 6.6e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTA 18

Db 24 GCATGCATGCATTATATA 7

RESULT 9

ACA23973/c

ID ACA23973 standard; DNA; 141 BP.

XX AC ACA23973;

XX DT 19-JUN-2003 (first entry)

XX XX Prokaryotic essential gene #5630.

XX DE Antisense; ds; prokaryotic essential gene; cell proliferation;

XX KW drug design; gene.

XX XX Borrelia cepacia.

XX OS W0200277183-A2.

XX PN

XX ED 03-OCT-2002.

XX XX

XX PF 21-MAR-2002; 2002WO-US009107.

XX XX

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX XX (ELIT-) ELITRA PHARM INC.

XX XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX XX WPI; 2003-029926/02.

XX DR P-PSDB; ABU20103.

XX XX

XX PT New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 14; SEQ ID NO 11843; 1766pp; English.

XX XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation or screening for homologous nucleic acids required  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX  
 SQ Sequence 141 BP; 28 A; 41 C; 51 G; 21 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 7; Length 141;  
 Best Local Similarity 84.2%; Pred. NO. 1.4e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19  
 |||||  
 Db 38 GCCTGCATGCATTACGGAC 20  
 |||||

RESULT 10  
 AAA69048/c  
 ID AAA69048 standard; DNA; 153 BP.  
 AC AAA69048;  
 XX

DT 06-AUG-2003 (revised)  
 DT 27-OCT-2000 (first entry)  
 XX

DE Bacteriophage 44AHJD nucleotide sequence 44HJDORP031.

XX Bacteriophage; antimicrobial; genome; identification; antibacterial;  
 KW bacterial growth inhibition; bacterial infection; ds.  
 XX

OS Staphylococcus phage 44AHJD.

XX WO200032825-A2.

XX 08-JUN-2000.

PF 03-DEC-1999; 99WO-IB002040.

XX 03-DEC-1998; 98US-0110992P.

PR 03-JUN-1999; 99US-00326144.

PR 28-SEP-1999; 99US-00407804.

PR 30-SEP-1999; 99US-0157218P.

PR 01-DEC-1999; 99US-0168777P.

XX 02-DEC-1999; 99US-00454252.

XX (PHAG-) PHAGETECH INC.

XX Pelletier J, Gros P, Dubow M;

XX WPI; 2000-412361/35.

XX P-PSDB; AAB16563.

XX Identifying a bacteriophage coding region for treating bacterial

XX infections comprises identifying a nucleic acid encoding a product that

XX inhibits bacteria when a bacteriophage infects a bacterium.

XX Example 9; Page 278; 456pp; English.

XX The present invention describes a method for identifying a bacteriophage

XX coding region encoding a product active on an essential bacterial target.

XX The method comprises identifying a nucleic acid sequence encoding a gene

XX product that provides a bacteria-inhibiting function when an

XX uncharacterised bacteriophage infects a pathogenic bacterium. The

CC compound active on a target of a bacteriophage inhibitor protein in a  
 CC bacteria is used to treat or prevent a bacterial infection in an animal.  
 CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage  
 CC nucleotide and protein sequences which are used in the exemplification of  
 CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX

SQ Sequence 153 BP; 52 A; 21 C; 27 G; 53 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 153;  
 Best Local Similarity 84.2%; Pred. NO. 1.4e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19  
 |||||  
 Db 70 GCATACCTGCATTACGTTTC 52  
 |||||

RESULT 11  
 AAV76005  
 ID AAV76005 standard; DNA; 162 BP.

XX AC AAV76005;

XX DT 16-MAR-1999 (first entry)

XX Staphylococcus aureus contig SEQ ID #1694.

XX Computer readable medium; vaccine; *S. aureus* infection; immunodetection;  
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
 KW skin infection; surgical wound infection; scalded skin syndrome;  
 XX toxic shock syndrome; ds.

OS Staphylococcus aureus.

XX EP786513-A2.

XX 30-JUL-1997.

PF 07-JAN-1997; 97EP-00100117.

XX 05-JAN-1996; 96US-0009861P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Rammon MR, Rosen CA;  
 XX WPI; 1997-374922/35.

XX Polynucleotide(s) and proteins derived from *Staphylococcus aureus* -

XX stored on computer readable medium and used in the production of anti-  
 XX *S. aureus* vaccines.

XX Claim 1; Page 2035; 3271pp; English.

XX This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences  
 CC of the invention. The DNA sequences are recorded on a computer readable  
 CC medium, preferably selected from a floppy or hard disk, random access  
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
 CC the *S. aureus* DNA sequences allows putative functions to be assigned so  
 CC that protein-encoding or regulatory regions of commercial, therapeutic or  
 CC industrial importance can be obtained. Specifically, sequences which are  
 CC likely to encode antigens have been identified and these polypeptides can  
 CC be used in a vaccine composition against *S. aureus* infection. The  
 CC polypeptides can also be used in a kit for the immunodetection of  
 CC *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases,  
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used  
 CC for recombinant production of the polypeptides. The new DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the *S. aureus* DNA sequences contained on the computer  
 CC readable medium

XX

SQ Sequence 162 BP; 46 A; 28 C; 33 G; 54 T; 0 U; 1 Other;  
 Query Match 69.0%; Score 13.8; DB 2; Length 162;  
 Best Local Similarity 88.2%; Pred. No. 2.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCATGCATTACGTACG 20  
 | | | | | | | | | | | | | | | | | | | | | |  
 DB 50 TACATGCAATACGTACG 66

RESULT 12  
 AAC21274/c  
 ID AAC21274 standard; cDNA; 196 BP.  
 XX  
 AC AAC21274;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 25349.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-00200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI; 2000-500381/45.  
 XX  
 CC New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 CC obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC  
 CC Claim 1; SEQ ID NO 25349; 71pp + Sequence Listing; English.  
 CC  
 CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'  
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used  
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in  
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC They are used to obtain upstream regulatory sequences and to design  
 CC expression and secretion vectors  
 CC  
 SQ Sequence 196 BP; 68 A; 35 C; 34 G; 58 T; 0 U; 1 Other;  
 Query Match 69.0%; Score 13.8; DB 3; Length 196;  
 Best Local Similarity 88.2%; Pred. No. 2.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19  
 | | | | | | | | | | | | | | | | | | | | | |  
 DB 31 ATGCATGCTTTATGTAC 15

RESULT 13

AAT29051  
 ID AAT29051 standard; DNA; 28 BP.  
 XX  
 AC AAT29051;  
 XX  
 DT 03-OCT-1996 (first entry)  
 XX  
 DE Maltogenic alpha-amylase signal peptide PCR primer DK16.  
 XX  
 KW Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis;  
 KW lytic enzyme; beta-glucan degradation; cell wall lysis; pigment;  
 KW colorant; flavour; yeast extract; protoplast; Oerskovia xanthineolytica;  
 KW polymerase chain reaction; primer; PCR; alpha-amylase; signal peptide;  
 KW Bacillus stearothermophilus; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9612013-A1.  
 XX  
 PD 25-APR-1996.  
 XX  
 PF 16-OCT-1995; 95WO-DK000414.  
 XX  
 PR 14-OCT-1994; 94DK-00001192.  
 XX  
 PA (NOVO ) NOVO-NORDISK AS.  
 XX  
 PI Ferrer P, Diers I, Hedegaard L, Halkier T, Aasenjo JA, Savva D;  
 XX  
 DR WPI; 1996-222000/22.  
 XX  
 CC DNA construct encoding enzyme with beta-1,3-glucanase activity - useful  
 CC for modifying or degrading beta-glucan contg. material and in the prepn.  
 CC of e.g. food colourants, flavourings and yeast extracts.  
 CC  
 CC Example 7; Page 22; 60pp; English.  
 CC  
 CC Primers DK15 (AAT29050) and DK16 (AAT29051) were used for the PCR  
 CC amplification of the ribosome binding site and signal peptide coding  
 CC regions of the Bacillus stearothermophilus maltogenic alpha-amylase gene  
 CC in pDN520. The PCR product was used to construct pPF1, which also  
 CC carried a gene (AAT29043) for Oerskovia xanthineolytica beta-1,3-  
 CC glucanase (AAR97362). Transformation of Bacillus subtilis strain DN1885  
 CC or protease-deficient strain Toc46 allowed prodn. of the Oerskovia lytic  
 CC enzyme  
 CC  
 SQ Sequence 28 BP; 10 A; 5 C; 8 G; 5 T; 0 U; 0 Other;  
 Query Match 68.0%; Score 13.6; DB 2; Length 28;  
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20  
 | | | | | | | | | | | | | | | | | | | | | |  
 DB 4 GCAAGCTTGCAATTACGAAAG 23

RESULT 14  
 AAQ95094  
 ID AAQ95094 standard; DNA; 76 BP.  
 XX  
 AC AAQ95094;  
 XX  
 DT 02-OCT-1995 (first entry)  
 XX  
 DE Configuration detecting nucleic acid probe #4.  
 XX  
 KW Probe; PCR; terminus; amplify; primer; configuration; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key primer\_bind 65..76  
 FT Location/Qualifiers

```
FT FT /*tag= a
XX /note= "PCR primer binding site"
PN JP06343498-A.
XX
XX 20-DEC-1994.
PD
XX PF 03-JUN-1993; 93JP-00133640.
XX PR 03-JUN-1993; 93JP-00133640.
XX PA (CANO ) CANON KK.
XX DR WPI; 1995-069322/10.
XX PT Nucleic acid probe - and method for detecting nucleic acid.
XX PS Example 1; Col 4; 6pp; Japanese.
XX CC Probes (AAQ95091-4) can be used in a method for the detection of a
CC nucleic acid target sequence which has PCR-controlled termini and can be
CC amplified by PCR. The probes can be used to detect configuration
XX SQ Sequence 76 BP; 18 A; 22 C; 23 G; 13 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 2; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTACGTACG 20
Db 53 GCATGCATGCATCGCGCG 72
RESULT 15
AAQ95094/c
ID AAQ95094 standard; DNA; 76 BP.
XX
XX AC AAQ95094;
XX
XX DT 02-OCT-1995 (first entry)
XX
XX DE Configuration detecting nucleic acid probe #4.
XX
XX KW Probe; PCR; terminus; amplify; primer; configuration; ss.
XX
XX OS Synthetic.
XX
XX EH Key Location/Qualifiers
FT primer_bind 65..76
FT FT /*tag= a
FT FT /note= "PCR primer binding site"
XX
XX PN JP06343498-A.
XX
XX PD 20-DEC-1994.
XX
XX PF 03-JUN-1993; 93JP-00133640.
XX PR 03-JUN-1993; 93JP-00133640.
XX PA (CANO ) CANON KK.
XX DR WPI; 1995-069322/10.
XX PT Nucleic acid probe - and method for detecting nucleic acid.
XX PS Example 1; Col 4; 6pp; Japanese.
XX CC Probes (AAQ95091-4) can be used in a method for the detection of a
CC nucleic acid target sequence which has PCR-controlled termini and can be
CC amplified by PCR. The probes can be used to detect configuration
XX
```

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SQ Sequence 76 BP; 18 A; 22 C; 23 G; 13 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 2; Length 76;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GCATGCATGCATTACGTACG 20
Db 26 GCATGCATGCATCGCGTCTCG 7
Search completed: August 11, 2004, 17:56:35
Job time : 292.366 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 16:50:49 ; Search time 2394.19 Seconds  
(without alignments)  
249.455 Million cell updates/sec

Title: US-09-540-843-8  
Perfect score: 20  
Sequence: 1 gcatgcattacgtacg 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0  
Maximum DB seq length: 200

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_png.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	85.0	110	28	AQ965378 LERIB78TR
2	15.8	79.0	127	14	CD725785 312 Penni
3	15.8	79.0	136	10	AW581082 RCI-LT005
4	15.8	79.0	142	10	AW935636 QV3-DT001

5	15.8	79.0	177	28	BZ411188
6	15.4	77.0	177	28	CC440642
7	15.4	77.0	199	10	BE833189
8	15.4	77.0	200	10	BB737705
9	15.2	76.0	137	28	CC434123
10	15.2	76.0	155	14	CF078438
11	15.2	76.0	165	28	BH866954
12	15.2	76.0	166	12	BJ250639
13	15.2	76.0	171	28	BH619747
14	15.2	76.0	182	29	CG408774
15	15.2	76.0	183	12	BM370416
16	15	75.0	109	12	BG266669
17	14.8	74.0	42	28	AZ771346
18	14.8	74.0	109	13	BQ613131
19	14.8	74.0	145	28	AZ114630
20	14.8	74.0	151	9	AW101085
21	14.8	74.0	154	10	BE939102
22	14.8	74.0	156	29	CG306670
23	14.8	74.0	162	10	BE058631
24	14.8	74.0	168	28	BH317050
25	14.8	74.0	178	28	BH870273
26	14.8	74.0	180	10	AW678292
27	14.8	74.0	191	14	CA820487
28	14.8	74.0	192	29	AG262468
29	14.4	72.0	119	12	B1119966
30	14.4	72.0	123	9	AI920345
31	14.2	71.0	92	28	B43951
32	14.2	71.0	103	14	W66964
33	14.2	71.0	116	13	BQ589121
34	14.2	71.0	119	12	BP014192
35	14.2	71.0	120	28	BZ586324
36	14.2	71.0	135	28	CC021359
37	14.2	71.0	135	29	CG935001
38	14.2	71.0	147	28	BZ419418
39	14.2	71.0	154	13	BX608931
40	14.2	71.0	156	9	AA129771
41	14.2	71.0	163	12	BG362444
42	14.2	71.0	167	10	BE076919
43	14.2	71.0	168	13	BW287445
44	14.2	71.0	170	10	AW787508
45	14.2	71.0	170	12	BG155382

## ALIGNMENTS

RESULT 1	AQ965378	110 bp	DNA	linear	GSS 28-JAN-2000	
LOCUS	LERIB78TR	LERG	Arabidopsis thaliana	genomic clone	LERIB78, genomic	
DEFINITION	survey sequence.					
ACCESSION	AQ965378					
VERSION	AQ965378.1	GI:6793079				
KEYWORDS	GSS.					
SOURCE	Arabidopsis thaliana (thale cress)					
ORGANISM	Arabidopsis thaliana					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
REFERENCE	1 (bases 1 to 110)					
AUTHORS	Buell,C.R.; Lin,X.; Pai,G.; Barnstead,M.; Bowman,C.; Utterbach,T.; Feldblyum,T.; Liang,F.; Creasy,T. and Fraser,C.M.					
TITLE	Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Xiaoying Lin The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: at@tigr.org For additional information, see <a href="http://www.tigr.org/tcdb/at/at.html">http://www.tigr.org/tcdb/at/at.html</a>					

BZ411188	OGACT10TC
CC440642	PUHGV17TB
BE833189	QV3-OT006
BB737705	BB737705
CC434123	PUHJB43TB
CF078438	QHK2H04.Y
BH866954	bg92c06.Y
BJ250639	BJ250639
BH619747	1007062C1
CG408774	D8467 Ds
BM370416	EBR008 SQ
BG266669	1000099F0
AZ771346	1M0573M21
BQ613131	8BP83el2.
AZ114630	REC1-23-4
AW101085	sd73906.Y
BE939102	PM2-TN012
CG306670	CGXBR88TH
BE058631	sn18f11.Y
BH317050	CH230-131
BH870273	hm59f07.G
AW678292	WS1_14.D0
CA820487	sau83g12.
AG262468	Lotus cor
B1119966	F007P93Y
AI920345	603019F04
B43951	HS-1058-B1-
W66964	me29a10.r1
BQ589121	S013715-0
BP014192	BP014192
BZ586324	3590_1_16
CC021359	3590_1_24
CG935001	MBECA46TF
BZ419418	if53f12.b
BX608931	EX608931
AA129771	zoi3c12.r
BG362444	qb72d06.Y
BE076919	CM1-BT060
BW287445	BW287445
AW787508	945010B04
BG155382	sab42g06.

Seq primer: TR  
Class: shotgun.

FEATURES  
source  
1..110  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="LANDSBERG ERECTA"  
/db\_xref="taxon:3702"  
/clone="LERIB78"  
/clone\_lib="LERG"  
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation."

## ORIGIN

Query Match 85.0%; Score 17; DB 28; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGT 17  
|||||  
Db 31 GCATGCATGCATTACGT 47

## RESULT 2

CD725785 127 bp mRNA linear EST 26-JUN-2003  
LOCUS 312 Pennisetum glaucum seedlings exposed to salt (500 mM NaCl)  
DEFINITION Pennisetum glaucum cDNA clone 312, mRNA sequence.  
ACCESSION CD725785  
VERSION CD725785.1 GI:32276632  
KEYWORDS EST.  
SOURCE Pennisetum glaucum  
ORGANISM Pennisetum glaucum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Paniceae; Pennisetum.

REFERENCE 1 (bases 1 to 127)  
AUTHORS Mishra,R.N., Markandeya,G., Nair,S., Reddy,A.R., Sopory,S.K. and Reddy,M.K.

TITLE Analysis of Expressed Sequence Tags from a subtracted cDNA library prepared from Pennisetum glaucum seedlings that were exposed to salt (500 mM NaCl) stress

JOURNAL Unpublished (2003)  
COMMENT Contact: Reddy MK  
Plant Molecular Biology Laboratory  
International Centre for Genetic Engineering and Biotechnology (ICGEB)

Aruna Asaf Ali Marg, New Delhi 110067, INDIA  
Tel: 91-11-26181242  
Fax: 91-11-26162316  
Email: redy@icgeb.res.in.

## FEATURES

source  
1..127  
/organism="Pennisetum glaucum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4543"  
/clone="312"  
/tissue\_type="Entire leaf tissue"  
/dev\_stage="Two-week-old seedlings"  
/clone\_lib="Pennisetum glaucum seedlings exposed to salt (500 mM NaCl)"  
/note="Organ: Leaf; Vector: Lambda Zap; Site 1: EcoRI; Site 2: XhoI"

## ORIGIN

Query Match 79.0%; Score 15.8; DB 14; Length 127;  
Best Local Similarity 89.5%; Pred. No. 5.1e+03; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19  
|||||

Db 46 GCATGCATGCATTACGCAC 64  
|||||

## RESULT 3

AW581082 136 bp mRNA linear EST 16-MAR-2000  
LOCUS RC1-LT0056-070100-011-all LT0056 Homo sapiens cDNA, mRNA sequence.  
DEFINITION AW581082  
ACCESSION AW581082  
VERSION AW581082.1 GI:7256131  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 136)  
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-27049322

Fax: +55-11-2707001

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-LT0056-070100-011-all&t3=2000-01-07&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 136.

## FEATURES

source

1..136  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="LT0056"  
/note="Organ: leiocios; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 10; Length 136;  
Best Local Similarity 89.5%; Pred. No. 5.2e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTACG 20  
|||||

Db 8 CATGCAGCATTACCTACG 26  
|||||

## RESULT 4

AW935636/c

LOCUS QV3-D0012-081299-021-f04 DT0012 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW935636

ACCESSION AW935636

VERSION AW935636.1 GI:8111042

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 142)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and



```

DEFINITION QV3-OT0063-120700-263-h06 OT0063 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE833189
VERSION BE833189.1 GI:10265567
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 199)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=6t2=QV3-OT0063-120
700-263-h06&t3=2000-07-12&t4=1)
Seg primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 199.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="OT0063"
/Note="Organ: ovary; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
ORIGIN
Query Match 77.0%; Score 15.4; DB 10; Length 199;
Best Local Similarity 94.1%; Pred. No. 8.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CATGCATGCATTACGTA 18
Db 164 CATTTCATGCATTACGTA 180
RESULT 8
BB737705/c
LOCUS BB737705
DEFINITION BB737705 RIKEN full-length enriched, 6 days neonate spleen Mus
musculus cDNA clone F430015B13 3', mRNA sequence.
ACCESSION BB737705
VERSION BB737705.1 GI:16136855
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 200)

```

## AUTHORS

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Mateuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,K., Sakai,C., Sakai,K., Sakazume,N., Sakaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

## TITLE

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
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Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Kira,A., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.  
e mouse tissues.

## FEATURES

Location/Qualifiers  
1..200  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="F430015B13"  
/tissue type="spleen"  
/dev stage="6 days neonate"  
/clone\_lib="RIKEN full-length enriched, 6 days neonate spleen"

## ORIGIN

Query Match 77.0%; Score 15.4; DB 10; Length 200;  
Best Local Similarity 94.1%; Pred. No. 8.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTA 18

Db 93 CATGCATGCATTACGTA 77

## RESULT 9

CC434123/c

LOCUS CC434123

DEFINITION CC434123

genomic survey sequence.

ACCESSION CC434123

VERSION CC434123.1

KEYWORDS GSS

SOURCE Zea mays

ORGANISM Zea mays

CC434123 137 bp DNA linear GSS 20-MAY-2003  
F003437B\_ZM\_0.6\_1.0 KB Zea mays genomic clone ZMMBTa62H14,

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 137)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennettzen,J.

## TITLE

Maize Genomics Consortium

## JOURNAL

Unpublished (2003)

## COMMENT

Other GSSs: PUHJB43TD

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

## FEATURES

Location/Qualifiers

1..137

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/mol\_type="genomic DNA"

/strain="B73"

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/clone\_lib="ZM 0.6-1.0 kb"

/notes="vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high

Cor selected genomic DNA library"

## ORIGIN

Query Match 76.0%; Score 15.2; DB 28; Length 137;  
Best Local Similarity 85.0%; Pred. No. 9.6e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## QY

1 GCATGCATGCATTACTACG 20

## Db

70 GCATGCATGCATTACTACG 51

## RESULT 10

CF078438

LOCUS

DEFINITION OHK2H04.YG.ab1 OH K sunflower H.paradoxus Helianthus paradoxus cDNA clone OHK2H04, mRNA sequence.

ACCESSION CF078438

VERSION CF078438.1 GI:33117481

KEYWORDS EST.

SOURCE Helianthus paradoxus

ORGANISM Helianthus paradoxus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroidae; Heliantheae; Helianthus.

## REFERENCE

AUTHORS

Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Latelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.

TITLE

Letuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/

JOURNAL

Unpublished (2002)

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]

Department of Vegetable Crops, R.W.Michelmore Lab

University of California at Davis (UCD)

Asmundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]

Singleton, see http://cgpdb.ucdavis.edu/ for details.

Plate: QHK2

row: H

column: 04.

Location/Qualifiers

1..155

/organism="Helianthus paradoxus"

/mol\_type="mRNA"

/db\_xref="taxon:73304"

/clone="QHK2H04"

/lab\_host="E.coli"

/clone\_lib="OH K sunflower H.paradoxus"

/notes="Vector: pBRCNASFIAB; The library was constructed

from four different sources (seedling, root, leaf and

flower) of RNA from a single genotype. cDNAs were pooled

and directionally cloned into a custom medium-copy vector.

Details of library construction can be obtained at

http://cgpdb.ucdavis.edu/"

## ORIGIN

Query Match 76.0%; Score 15.2; DB 14; Length 155;  
Best Local Similarity 85.0%; Pred. No. 9.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## QY

1 GCATGCATGCATTACGTACG 20

## Db

102 GCATGCATGCATCGCTAAG 121

## RESULT 11

BH866954

LOCUS

DEFINITION hg92c06.y8 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays genomic clone hg92c06 5', genomic survey sequence.

ACCESSION BH866954

VERSION BH866954.1 GI:22102851

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

1 (bases 1 to 165)  
Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., McCombie,W.R. and Martienssen,R.A.

Genomic shotgun sequences from Zea mays (methyl-filtered)

Unpublished (2002)

TITLE

JOURNAL

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hg92 row: c column: 06

Seq primer: -21M13UnivRev

Class: shotgun

High quality sequence stop: 165.

Location/Qualifiers

1..165

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone="hg92c06"

/lab\_host="JM107 or DH5a"

/clone\_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"

/notes="Organ: Immature ears; Site 1: Xba I; Site 2: Xba I;

The vector was digested with XbaI and one nucleotide was

added by fill in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size

fractionated using sephadex. The resulting fragments were

between 0.8 and 3 kb and were cloned into the vector

(.x/y reads in M13mp19, .b/g reads in pUC19). The same

ligation was transformed in either JM107 or DH5a."

## ORIGIN

Query Match 76.0%; Score 15.2; DB 28; Length 165;  
Best Local Similarity 85.0%; Pred. No. 1e+04;

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
    ||||| || |||||
Db 141 GCATGCACGCTGACGTACG 160

RESULT 12
BJ250639/c
LOCUS BJ250639 166 bp mRNA linear EST 05-APR-2002
DEFINITION BJ250639 Y. Ogiwara unpublished cDNA library, Wh_f Triticum
aestivum cDNA clone whf16104 3', mRNA sequence.
ACCESSION BJ250639
VERSION BJ250639.1 GI:20060605
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 166)
AUTHORS Ogiwara, Y. and Murai, K.
JOURNAL Expressed genes in Triticum aestivum
COMMENT Unpublished (2002)
Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
    source
        1..166
            /organism="Triticum aestivum"
            /mol_type="mRNA"
            /culturvar="Chinese Spring"
            /db_xref="taxon:4565"
            /clone="whf16104"
            /tissue_type="spike at flowering date"
            /dev_stage="Feekes' scale 10.5.1"
            /clone_lib="Y. Ogiwara unpublished cDNA library, Wh_f"

ORIGIN
    Query Match 76.0%; Score 15.2; DB 12; Length 166;
    Best Local Similarity 85.0%; Pred. No. 1e+04;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
    ||||| || |||||
Db 131 GCATGCATGTATTGGGTGG 112

RESULT 13
BH619747
LOCUS BH619747 171 bp DNA linear GSS 30-JAN-2002
DEFINITION 1007062C12.2EL y1 1007 - RescueMu Grid H Zea mays genomic
survey sequence.
ACCESSION BH619747
VERSION BH619747.1 GI:18430811
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 171)
AUTHORS Walbot, V.
JOURNAL Maize genomic sequences found using engineered RescueMu transposon
COMMENT Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA

```

```

Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007062 column: 18
Class: transposon-tagged.
Location/Qualifiers
    1..171
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /culturvar="mixed background W23/A188/B73"
        /db_xref="taxon:4577"
        /tissue_type="leaf"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="1007 - RescueMu Grid H"
        /organ="Organ: leaf; Vector: RescueMu (engineered from
        pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
        RescueMu is a 4.9 kb, modified maize Mu transposon
        designed to allow plasmid rescue from total genomic DNA.
        Mu elements insert preferentially into transcription web
        units. For more information on RescueMu, go to the web
        site 'www.zmdb.iastate.edu' and follow the links for
        'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
        was extracted from leaf punches, double digested using
        BamHI and BglII, and ligated to form circular plasmids.
        DH10B cells were transformed and then screened on LB
        plates with ampicillin."

ORIGIN
    Query Match 76.0%; Score 15.2; DB 28; Length 171;
    Best Local Similarity 85.0%; Pred. No. 1e+04;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
    ||||| || |||||
Db 40 GCATGCATGCATCAGCAATG 59

RESULT 14
CG408774/c
LOCUS CG408774 182 bp DNA linear GSS 03-SEP-2003
DEFINITION Ds467 Ds insertion lines Oryza sativa (japonica cultivar-group)
genomic, genomic survey sequence.
ACCESSION CG408774
VERSION CG408774.1 GI:34430139
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 182)
AUTHORS Kim, C.M., Piao, H.L., Park, S.J., Chon, N.S., Je, B.I., Sun, B.,
Park, S.H., Park, J.Y., Lee, E.J., Kim, M.J., Lee, J.J., Nam, M.H.,
Eun, M.Y. and Han, C.D.
JOURNAL Rapid, large-scale generation of Ds transposant lines and analysis
COMMENT Unpublished (2003)
Contact: Chang-deok Han
Division of Applied Life Science, PMBRC
Gyeongsang National University
Gazwa-dong 900, Jinju 660-701, South Korea
Tel: +82 55 751 6029
Fax: +82 55 759 9363
Email: cdhan@nongae.gsnu.ac.kr
Location: chromosome 3 clone OSUNBb0011G21
Class: transposon-tagged.
Location/Qualifiers
    1..182
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="genomic DNA"

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Job time : 2400.86 secs

/cultivar="Dongjin"  
/db\_xref="taxon:39947"  
/clone\_lib="Ds insertion lines"

## ORIGIN

Query Match 76.0%; Score 15.2; DB 29; Length 182;  
Best Local Similarity 85.0%; Pred. No. 1e+04; 3; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20

Db 118 GCATGCATGCATGACACACG 99

## RESULT 15

BM370416

LOCUS

DEFINITION

BM370416 183 bp mRNA linear EST 23-JUL-2002  
EBro08\_SQ004 C17 R root, 3 week, drought-stressed, cv Optic, EBro08  
Hordeum vulgare subsp. vulgare cDNA clone EBro08\_SQ004\_C17 5', mRNA  
sequence.

ACCESSION

BM370416

VERSION

BM370416.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Hordeum vulgare subsp. vulgare  
Hordeum vulgare subsp. vulgare  
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticeae; Hordeum.  
1 (bases 1 to 183)  
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,  
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.  
Development of Barley Transcriptome Resources  
Unpublished (2001)  
Contact: Waugh R, Marshall DF  
Genome Dynamics/Computational Biology  
Scottish Crop Research Institute  
Invergowrie, Dundee, DD2 5DA, Scotland, UK  
Tel: 00 44 1382 562731  
Fax: 00 44 1382 562426  
Email: est@scri.sari.ac.uk

All sequence has a Phred quality score of 20 or over

Seq primer: M13 reverse.

## FEATURES

source

1..183

Location/Qualifiers

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Optic"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="EBro08\_SQ004\_C17"

/tissue\_type="root"

/dev\_stage="3 week"

/lab\_host="DH10B"

/clone\_lib="root, 3 week, drought-stressed, cv Optic,  
EBro08"

/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;  
Non-normalised library, directionally cloned into pSPORT1.  
Derived from roots of 3 week old drought stressed barley  
plants. Developed as part of the barley transcriptome  
resources of BBSRC/SEERAD funded cereal IGF (Investigating  
Gene Function) project."

## ORIGIN

Query Match 76.0%; Score 15.2; DB 12; Length 183;  
Best Local Similarity 85.0%; Pred. No. 1e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20

Db 116 GCATTCATGTACTACGTACG 135

Search completed: August 11, 2004, 18:58:49

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:57:26 ; Search time 60 Seconds  
(without alignments)  
184.984 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcatgattacgtaag 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.8	69.0	162	4	US-08-956-171B-1694
2	13.6	68.0	58	1	US-07-982-712-34
3	13.6	68.0	58	1	US-07-982-712-35
4	13.4	67.0	28	1	US-08-053-564-10
5	13.4	67.0	42	1	US-08-301-872A-6
6	13.4	67.0	42	2	US-08-443-372A-6
7	13.4	67.0	70	1	US-08-301-872A-7
8	13.4	67.0	70	1	US-08-301-872A-8
9	13.4	67.0	70	2	US-08-443-372A-7
10	13.4	67.0	70	2	US-08-443-372A-8
11	13.2	66.0	33	4	US-09-535-851A-6
12	13.2	66.0	177	4	US-09-313-294A-292
13	12.6	63.0	26	1	US-07-720-586-7
14	12.6	63.0	65	3	US-09-415-522-24
15	12.6	63.0	108	4	US-08-956-171B-4834
16	12.6	63.0	129	4	US-08-956-171B-4790
17	12.6	63.0	178	4	US-09-313-294A-26
18	12.4	62.0	38	2	US-09-097-759-6
19	12.4	62.0	38	3	US-09-065-104-24
20	12.4	62.0	59	2	US-08-816-155B-23
21	12.4	62.0	59	3	US-08-815-809-8
22	12.4	62.0	59	3	US-09-079-587-23
23	12.4	62.0	138	1	US-08-600-234-5
24	12.4	62.0	138	1	US-08-386-921-5
25	12.4	62.0	141	1	US-08-386-921-13
26	12.4	62.0	144	1	US-08-386-921-11
27	12.4	62.0	147	1	US-08-386-921-9

C 28	12.4	62.0	161	1	US-08-600-234-2	Sequence 2, Appli
C 29	12.4	62.0	161	1	US-08-386-921-2	Sequence 2, Appli
C 30	12.4	62.0	161	1	US-08-386-921-10	Sequence 10, Appli
C 31	12.4	62.0	197	1	US-08-386-921-4	Sequence 4, Appli
C 32	12.2	61.0	20	4	US-08-234-312B-21	Sequence 21, Appli
C 33	12.2	61.0	20	4	US-08-468-024B-21	Sequence 21, Appli
C 34	12.2	61.0	20	4	US-08-465-679-21	Sequence 21, Appli
C 35	12.2	61.0	21	4	US-08-187-757D-19	Sequence 19, Appli
C 36	12.2	61.0	21	4	US-08-210-143C-19	Sequence 19, Appli
C 37	12.2	61.0	30	4	US-09-504-358-43	Sequence 43, Appli
C 38	12.2	61.0	30	4	US-09-954-314-43	Sequence 43, Appli
C 39	12.2	61.0	35	4	US-09-122-315C-15	Sequence 15, Appli
C 40	12.2	61.0	35	4	US-09-360-376-4	Sequence 4, Appli
C 41	12.2	61.0	39	2	US-08-452-724A-18	Sequence 18, Appli
C 42	12.2	61.0	39	4	US-08-453-623-18	Sequence 18, Appli
C 43	12.2	61.0	43	3	US-08-961-810-31	Sequence 31, Appli
C 44	12.2	61.0	43	3	US-08-352-902D-31	Sequence 31, Appli
C 45	12.2	61.0	43	4	US-09-265-503B-31	Sequence 31, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-956-171B-1694  
; Sequence 1694, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 1694:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

US-08-956-171E-1694

Query Match 69.0%; Score 13.8; DB 4; Length 162;  
Best Local Similarity 88.2%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCATGCATTACGTACG 20  
Db 50 TACATGCAATACGTACG 66

RESULT 2  
US-07-982-712-34  
US-07-982-712-34 Application US/07982712  
Sequence 34, Application US/07982712  
Patent No. 5436391  
GENERAL INFORMATION:  
APPLICANT: Hideya FUJIMOTO, Kimiko ITOH  
APPLICANT: Mikihiko YAMAMOTO, and Ko SHIMAMOTO  
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous  
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/982,712  
FILING DATE: 19921127  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-07-982-712-34

Query Match 68.0%; Score 13.6; DB 1; Length 59;  
Best Local Similarity 80.0%; Pred. No. 3.7e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20  
Db 9 GCATGCATGAATTCCTAGG 28

RESULT 3  
US-07-982-712-35/c  
US-07-982-712-35/c Application US/07982712  
Sequence 35, Application US/07982712  
Patent No. 5436391  
GENERAL INFORMATION:  
APPLICANT: Hideya FUJIMOTO, Kimiko ITOH  
APPLICANT: Mikihiko YAMAMOTO, and Ko SHIMAMOTO  
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous  
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof

NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/982,712  
FILING DATE: 19921127  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-07-982-712-35

Query Match 68.0%; Score 13.6; DB 1; Length 58;  
Best Local Similarity 80.0%; Pred. No. 3.7e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20  
Db 54 GCATGCATGAATTCCTAGG 35

RESULT 4  
US-08-053-564-10/c  
US-08-053-564-10/c Application US/08053564  
Sequence 10, Application US/08053564  
Patent No. 5418153  
GENERAL INFORMATION:  
APPLICANT: MORI, MASASHI  
APPLICANT: OKUNO, TETSURO  
APPLICANT: FURUSAWA, IWAO  
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF  
TITLE OF INVENTION: EXOGENOUS GENE OR ITS PRODUCT  
TITLE OF INVENTION: IN PLANT CELLS NO.2  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
ADDRESSEE: Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version  
SOFTWARE: #1.25  
CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/053,564
/ FILING DATE: 28-APR-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP HEI-4-152593
/ FILING DATE: 28-APR-1992
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)293-7060
/ TELEFAX: (202)293-7860
/ TELEX: 649113
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Other nucleic acid
/ DESCRIPTION: synthesized oligonucleotide
US-08-053-564-10

Query Match 67.0%; Score 13.4; DB 1; Length 28;
Best Local Similarity 93.3%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACG 16
Db 20 CATGCATGCATTCG 6

RESULT 5
US-08-301-872A-6
; Sequence 6, Application US/08301872A
; Patent No. 580734
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Miller, Allan M.
; TITLE OF INVENTION: Library Screening Method
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,872A
; FILING DATE: 06-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/739,861
; FILING DATE: 02-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/552,183
; FILING DATE: 13-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT90-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-443-372A-6

Query Match 67.0%; Score 13.4; DB 2; Length 42;
Best Local Similarity 93.3%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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/ MOLECULE TYPE: DNA (genomic)
US-08-301-872A-6

Query Match 67.0%; Score 13.4; DB 1; Length 42;
Best Local Similarity 93.3%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCATGCATTACGTAC 19
Db 12 GGATGCATTACGTAC 26

RESULT 6
US-08-443-372A-6
; Sequence 6, Application US/08443372A
; Patent No. 5869239
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Miller, Allan M.
; TITLE OF INVENTION: Library Screening Method
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,372A
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/301,872
; FILING DATE: 06-SEP-1994
; APPLICATION NUMBER: US 07/739,861
; FILING DATE: 02-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/552,183
; FILING DATE: 13-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT90-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-443-372A-6

Query Match 67.0%; Score 13.4; DB 2; Length 42;
Best Local Similarity 93.3%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCATGCATTACGTAC 19
Db 12 GGATGCATTACGTAC 26

RESULT 7
US-08-301-872A-7/c
; Sequence 7, Application US/08301872A
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; Patent No. 5580734
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Miller, Allan M.
; TITLE OF INVENTION: Library Screening Method
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,872A
; FILING DATE: 06-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/739,861
; FILING DATE: 02-AUG-1991
; APPLICATION NUMBER: US 07/552,183
; FILING DATE: 13-JUL-1990
; NAME: Granahan, Patricia
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT90-01A2
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-301-872A-7

Query Match 67.0%; Score 13.4; DB 1; Length 70;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATGCATTACGTACG 20
Db 54 CATGCATTACGTAGG 40

RESULT 8
US-08-301-872A-8
; Sequence 8, Application US/08301872A
; Patent No. 5580734
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Miller, Allan M.
; TITLE OF INVENTION: Library Screening Method
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,872A
; FILING DATE: 06-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/739,861
; FILING DATE: 02-AUG-1991
; APPLICATION NUMBER: US 07/552,183
; FILING DATE: 13-JUL-1990
; NAME: Granahan, Patricia
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT90-01A2
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-301-872A-8

Query Match 67.0%; Score 13.4; DB 1; Length 70;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATGCATTACGTACG 20
Db 17 CATGCATTACGTAGG 31

RESULT 9
US-08-443-372A-7/c
; Sequence 7, Application US/08443372A
; Patent No. 5869239
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Miller, Allan M.
; TITLE OF INVENTION: Library Screening Method
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,372A
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/301,872
; FILING DATE: 06-SEP-1994
; APPLICATION NUMBER: US 07/739,861
; FILING DATE: 02-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/552,183
; FILING DATE: 13-JUL-1990
; NAME: Granahan, Patricia
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT90-01A2
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 70 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-443-372A-7

Query Match 67.0%; Score 13.4; DB 2; Length 70;  
Best Local Similarity 93.3%; Pred. No. 4.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATGCATTACGTAG 20  
Db 54 CATGCATTACGTAG 40  
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## RESULT 10

US-08-443-372A-8  
Sequence 8, Application US/08443372A  
Patent No. 5869239

## GENERAL INFORMATION:

APPLICANT: Treco, Douglas A.  
APPLICANT: Miller, Allan M.  
TITLE OF INVENTION: Library Screening Method  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,372A  
FILING DATE: 17-MAY-1995

## CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/301,872

FILING DATE: 06-SEP-1994

APPLICATION NUMBER: US 07/739,861

FILING DATE: 02-AUG-1991

PRIOR APPLICATION DATA: US 07/552,183

FILING DATE: 13-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: TKT90-01A2

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 70 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-443-372A-8

Query Match 67.0%; Score 13.4; DB 2; Length 70;  
Best Local Similarity 93.3%; Pred. No. 4.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATGCATTACGTAG 20  
Db 17 CATGCATTACGTAG 31  
|||||

## RESULT 11

US-09-535-851A-6  
Sequence 6, Application US/09535851A  
Patent No. 6528636

## GENERAL INFORMATION:

APPLICANT: Battelle Memorial Institute  
TITLE OF INVENTION: A Promoter Sequence of 3-Phosphoglycerate Kinase Gene 2 of Lactic  
Patent No. 6528636  
TITLE OF INVENTION: Producing Fungus Rhizopus Oryzae and a Method of Expressing a Gene  
FILE REFERENCE: E-1891B  
CURRENT APPLICATION NUMBER: US/09/535,851A  
CURRENT FILING DATE: 2000-03-27  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 6  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
US-09-535-851A-6

Query Match 66.0%; Score 13.2; DB 4; Length 33;  
Best Local Similarity 83.3%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTA 18  
Db 4 GCATGCATGATTTCATA 21  
|||||

## RESULT 12

US-09-313-294A-292/c  
Sequence 292, Application US/09313294A  
Patent No. 6476212

## GENERAL INFORMATION:

APPLICANT: Ito, Laura Y.  
APPLICANT: Ialugudi, Raghunath V.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
FILE REFERENCE: PL-0017 US  
CURRENT APPLICATION NUMBER: US/09/313,294A  
CURRENT FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 7600  
SOFTWARE: PERL Program  
SEQ ID NO 292  
LENGTH: 177  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6476212 700548929H1  
NAME/KEY: unsure  
LOCATION: 2, 6, 75-93  
OTHER INFORMATION: a, t, c, g, or other  
US-09-313-294A-292

Query Match 66.0%; Score 13.2; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 6.4e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTA 18  
Db 52 GCATGCATGCATGCCATA 35  
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RESULT 13  
US-07-720-586-7  
; Sequence 7, Application US/07720586  
; Patent No. 5232831  
; GENERAL INFORMATION:  
; APPLICANT: Curt Milliman  
; APPLICANT: Philip W. Hammond  
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES  
; TITLE OF INVENTION: TO STREPTOCOCCUS PYOGENES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19910628  
; APPLICATION NUMBER: US/07/720,586  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 193/121  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-07-720-586-7  
Query Match 63.0%; Score 12.6; DB 1; Length 26;  
Best Local Similarity 78.9%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 CATGCATGCATTACGTACG 20  
DB 3 CTGTCATGTATTAGGCACG 21  
RESULT 14  
US-09-415-522-24/c  
; Sequence 24, Application US/09415522A  
; Patent No. 6291660  
; GENERAL INFORMATION:  
; APPLICANT: Gaffney, Thomas  
; APPLICANT: Wendland, Juergen  
; APPLICANT: Philippsen, Peter  
; TITLE OF INVENTION: No. 6291660e1 Fungal Genes Required For No. 6291660mal Growth And  
; TITLE OF INVENTION: Development  
; FILE REFERENCE: CGC2046  
; CURRENT APPLICATION NUMBER: US/09/415,522A  
; CURRENT FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Primer  
US-09-415-522-24  
Query Match 63.0%; Score 12.6; DB 3; Length 65;  
Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GCATGCATGCATTACGTAC 19  
DB 57 GCTTGCATGCCTTTCATAC 39  
RESULT 15  
US-08-956-171E-4834/c  
; Sequence 4834, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; APPLICANT: Gil H. Choi  
; APPLICANT: Patrick S. Dillon  
; APPLICANT: Craig A. Rosen  
; APPLICANT: Steven C. Barash  
; APPLICANT: Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,171E  
; FILING DATE: 20-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 4834:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4834:  
US-08-956-171E-4834  
Query Match 63.0%; Score 12.6; DB 4; Length 108;  
Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 CATGCATGCATTACGTACG 20  
DB 40 CTGTCATGTATTAGGCACG 22

US-09-540-843-8.szlm200.rni  
Query Match 63.0%; Score 12.6; DB 1; Length 26;  
Best Local Similarity 78.9%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 CATGCATGCATTACGTACG 20  
DB 3 CTGTCATGTATTAGGCACG 21  
RESULT 14  
US-09-415-522-24/c  
; Sequence 24, Application US/09415522A  
; Patent No. 6291660  
; GENERAL INFORMATION:  
; APPLICANT: Gaffney, Thomas  
; APPLICANT: Wendland, Juergen  
; APPLICANT: Philippsen, Peter  
; TITLE OF INVENTION: No. 6291660e1 Fungal Genes Required For No. 6291660mal Growth And  
; TITLE OF INVENTION: Development  
; FILE REFERENCE: CGC2046  
; CURRENT APPLICATION NUMBER: US/09/415,522A  
; CURRENT FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Primer  
US-09-415-522-24  
Query Match 63.0%; Score 12.6; DB 3; Length 65;  
Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GCATGCATGCATTACGTAC 19  
DB 57 GCTTGCATGCCTTTCATAC 39  
RESULT 15  
US-08-956-171E-4834/c  
; Sequence 4834, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; APPLICANT: Gil H. Choi  
; APPLICANT: Patrick S. Dillon  
; APPLICANT: Craig A. Rosen  
; APPLICANT: Steven C. Barash  
; APPLICANT: Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,171E  
; FILING DATE: 20-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 4834:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4834:  
US-08-956-171E-4834  
Query Match 63.0%; Score 12.6; DB 4; Length 108;  
Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 CATGCATGCATTACGTACG 20  
DB 40 CTGTCATGTATTAGGCACG 22

Thu Aug 12 09:23:33 2004

us-09-540-843-8.szlm200.rni

Page 7

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
340.279 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcattacacgtacg 20

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Total number of hits satisfying chosen parameters: 2263564

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Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	15	US-10-122-630-8
2	20	100.0	20	15	US-10-122-633-8
C 3	14.2	71.0	141	13	US-10-282-122A-11843
C 4	14.2	71.0	153	12	US-09-727-892-32
C 5	14.2	71.0	175	17	US-10-437-963-71654
C 6	14.2	71.0	191	17	US-10-437-963-32687
7	13.8	69.0	162	8	US-08-781-986A-1694
8	13.8	69.0	162	13	US-10-329-624-1694
9	13.8	69.0	173	13	US-10-424-599-76449
10	13.8	69.0	177	13	US-10-424-599-1569
C 11	13.8	69.0	180	13	US-10-424-599-59127
12	13.8	69.0	187	13	US-10-424-599-76527
13	13.6	68.0	112	17	US-10-437-963-46744
C 14	13.6	68.0	165	13	US-10-085-783A-18933

C 15	13.6	68.0	165	16	US-10-242-535A-18933
16	13.6	68.0	179	17	US-10-437-963-87658
17	13.6	68.0	187	17	US-10-021-323-16957
C 18	13.4	67.0	175	9	US-09-728-444-656
C 19	13.4	67.0	188	13	US-10-424-599-129131
C 20	13.2	66.0	99	9	US-09-969-373-431
C 21	13.2	66.0	99	9	US-09-969-373-516
C 22	13.2	66.0	128	13	US-10-424-599-65688
C 23	13.2	66.0	131	17	US-10-437-963-96687
C 24	13.2	66.0	138	16	US-10-260-238-5712
25	13.2	66.0	139	13	US-10-085-783A-6262
26	13.2	66.0	139	16	US-10-242-535A-6262
27	13.2	66.0	157	13	US-10-424-599-66570
28	13.2	66.0	188	13	US-10-424-599-32750
C 29	13	65.0	17	15	US-10-194-035-95
30	13	65.0	106	9	US-09-969-373-854
31	13	65.0	106	9	US-09-969-373-855
C 32	13	65.0	109	9	US-09-969-373-494
C 33	13	65.0	130	9	US-09-234-093B-5343
34	13	65.0	150	10	US-09-754-853A-76
35	13	65.0	150	10	US-09-754-853A-78
C 36	13	65.0	182	9	US-09-923-876-2073
C 37	13	65.0	182	11	US-09-923-876-2073
C 38	12.8	64.0	60	10	US-09-908-975-10266
39	12.8	64.0	100	9	US-09-969-373-168
C 40	12.8	64.0	111	17	US-10-437-963-20497
C 41	12.8	64.0	145	13	US-10-424-599-59525
42	12.8	64.0	149	13	US-10-424-599-62748
C 43	12.8	64.0	172	13	US-10-424-599-48011
44	12.8	64.0	190	9	US-09-969-373-169
45	12.6	63.0	50	13	US-10-147-368-4

#### ALIGNMENTS

RESULT 1  
US-10-122-630-8  
; Sequence 8, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Year, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-8

Query Match 100.0%; Score 20; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTACG 20  
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Db 1 GCATGCATGCATTACGTACG 20

## RESULT 2

US-10-122-633-8  
; Sequence 8, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-8

Query Match 100.0%; Score 20; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0;

QY 1 GCATGCATGCATTACGTACG 20  
|||||  
Db 1 GCATGCATGCATTACGTACG 20

## RESULT 3

US-10-282-122A-11843/c  
; Sequence 11843, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Cart, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 11843  
; LENGTH: 141  
; TYPE: DNA  
; ORGANISM: Burkholderia cepacia  
US-10-282-122A-11843

Query Match 71.0%; Score 14.2; DB 13; Length 141;  
Best Local Similarity 84.2%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19  
|||||  
Db 38 GCCTGCATGCAATACGGAC 20

## RESULT 4

US-09-727-892-32/c  
; Sequence 32, Application US/09727892  
; Publication No. US20040091856A1  
; GENERAL INFORMATION:  
; APPLICANT: Phagotech, Inc.  
; APPLICANT: PELLETIER, Jerry  
; APPLICANT: GROS, Philippe  
; APPLICANT: DUBOW, Michael  
; TITLE OF INVENTION: DNA SEQUENCES FROM STAPHYLOCOCCUS AUREUS BACTERIOPHAGE 44 AHJD  
; FILE REFERENCE: 073406-0302  
; CURRENT APPLICATION NUMBER: US/09/727,892  
; CURRENT FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 32  
; LENGTH: 153  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus Bacteriophage 44 AHJD  
US-09-727-892-32

Query Match 71.0%; Score 14.2; DB 12; Length 153;  
Best Local Similarity 84.2%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGTAC 19  
|||||  
Db 70 GCATACCTGCATTACGTTTC 52

## RESULT 5

US-10-437-963-71654/c  
; Sequence 71654, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement



; REFERENCE/DOCKET NUMBER: PB248P1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 1694:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 162 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1694:  
US-10-329-624-1694

Query Match 69.0%; Score 13.8; DB 13; Length 162;  
Best Local Similarity 88.2%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGCATGCATTACGTACG 20  
DB 50 TACATGCATTACGTACG 66

RESULT 9  
US-10-424-599-76449  
; Sequence 76449, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 76449  
; LENGTH: 173  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_40045C.1  
US-10-424-599-76449

Query Match 69.0%; Score 13.8; DB 13; Length 173;  
Best Local Similarity 88.2%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19  
DB 48 ATGCATGCATTACAGAC 64

RESULT 10  
US-10-424-599-1569  
; Sequence 1569, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 1569  
; LENGTH: 177  
; TYPE: DNA  
; ORGANISM: Glycine max

; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_101416C.1  
US-10-424-599-1569

Query Match 69.0%; Score 13.8; DB 13; Length 177;  
Best Local Similarity 88.2%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19  
DB 98 ATGCATCCATTACTTAC 114

RESULT 11  
US-10-424-599-59127/c  
; Sequence 59127, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 59127  
; LENGTH: 180  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_24402C.1  
US-10-424-599-59127

Query Match 69.0%; Score 13.8; DB 13; Length 180;  
Best Local Similarity 88.2%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGT 17  
DB 178 GCATCCATGCATTGCGT 162

RESULT 12  
US-10-424-599-76527  
; Sequence 76527, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 76527  
; LENGTH: 187  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(187)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_40115C.1  
US-10-424-599-76527

Query Match 69.0%; Score 13.8; DB 13; Length 187;

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Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGCATGCATTACGTACG 20
Db 90 TGCATGCATTGCCTACG 106

RESULT 13
US-10-437-963-46744
; Sequence 46744, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 46744
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_49581C.1
US-10-437-963-46744

Query Match 68.0%; Score 13.6; DB 17; Length 112;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
Db 1 GCAAGCAACATTACGTAAAG 20

RESULT 14
US-10-085-783A-18933/c
; Sequence 18933, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: Liew, C.C.
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18933
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-18933

Query Match 68.0%; Score 13.6; DB 13; Length 165;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 GCATGCATGCATTACGTACG 20
Db 65 GCTTTCATGCATTACCTAAG 46

RESULT 15
US-10-242-535A-18933/c
; Sequence 18933, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18933
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-18933

Query Match 68.0%; Score 13.6; DB 16; Length 165;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATTACGTACG 20
Db 65 GCTTTCATGCATTACCTAAG 46

Search completed: August 11, 2004, 21:11:07
Job time : 289.72 secs
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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:38:14 ; Search time 317.419 Seconds  
(without alignments)  
682.741 Million cell updates/sec

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 catac 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_cm.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

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32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rnd.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	5	100.0	5	6	AX268756	AX268756 Sequence
C 2	5	100.0	5	6	AX268758	AX268758 Sequence
C 3	5	100.0	7	6	AX268755	AX268755 Sequence
C 4	5	100.0	7	6	AX268759	AX268759 Sequence
C 5	5	100.0	8	6	AX047565	AX047565 Sequence
C 6	5	100.0	8	6	AX104946	AX104946 Sequence
C 7	5	100.0	8	6	AX119567	AX119567 Sequence
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C 9	5	100.0	8	6	BD191357	BD191357 DNA-based
C 10	5	100.0	9	6	AX268753	AX268753 Sequence
C 11	5	100.0	9	6	AX667174	AX667174 Sequence
C 12	5	100.0	9	6	AX668771	AX668771 Sequence
C 13	5	100.0	9	6	AX668807	AX668807 Sequence
C 14	5	100.0	9	6	AX805897	AX805897 Sequence
C 15	5	100.0	9	9	S50583	S50583 type I proc
C 16	5	100.0	9	9	S50585	S50585 type I proc
C 17	5	100.0	10	6	AR8263	AR8263 oligonucleo
C 18	5	100.0	10	6	AR065157	AR065157 Sequence
C 19	5	100.0	10	6	AR079101	AR079101 Sequence
C 20	5	100.0	10	6	AR079103	AR079103 Sequence
C 21	5	100.0	10	6	AR098909	AR098909 Sequence
C 22	5	100.0	10	6	AR107335	AR107335 Sequence
C 23	5	100.0	10	6	AR107344	AR107344 Sequence
C 24	5	100.0	10	6	AR123039	AR123039 Sequence
C 25	5	100.0	10	6	AR136787	AR136787 Sequence
C 26	5	100.0	10	6	AR160130	AR160130 Sequence
C 27	5	100.0	10	6	BD238584	BD238584 Preparati
C 28	5	100.0	10	6	BD238895	BD238895 Preparati
C 29	5	100.0	10	6	BD239131	BD239131 Preparati
C 30	5	100.0	10	6	BD239305	BD239305 Preparati
C 31	5	100.0	10	6	BD239348	BD239348 Preparati
C 32	5	100.0	10	6	BD239406	BD239406 Preparati
C 33	5	100.0	10	6	BD239561	BD239561 Preparati
C 34	5	100.0	10	6	BD239605	BD239605 Preparati
C 35	5	100.0	10	6	BD239634	BD239634 Preparati
C 36	5	100.0	10	6	BD239635	BD239635 Preparati
C 37	5	100.0	10	6	BD239716	BD239716 Preparati
C 38	5	100.0	10	6	BD239837	BD239837 Preparati
C 39	5	100.0	10	6	BD240005	BD240005 Preparati
C 40	5	100.0	10	6	BD240133	BD240133 Preparati
C 41	5	100.0	10	6	BD240148	BD240148 Preparati
C 42	5	100.0	10	6	BD240243	BD240243 Preparati
C 43	5	100.0	10	6	BD240280	BD240280 Preparati
C 44	5	100.0	10	6	BD240281	BD240281 Preparati
C 45	5	100.0	10	6	BD240306	BD240306 Preparati

# ALIGNMENTS

RESULT 1  
AX268756/c  
LOCUS AX268756  
DEFINITION Sequence 4 from Patent WO0174342.  
ACCESSION AX268756  
VERSION AX268756.1 GI:16541828  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Gilchrist, B.A., Yaar, M. and Eller, M.  
TITLE Use of locally applied dna fragments  
JOURNAL Patent: WO 0174342-A 4 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)

AX268756 5 bp DNA  
Sequence 4 from Patent WO0174342.  
AX268756.1 GI:16541828  
synthetic construct  
synthetic construct  
artificial sequences.  
1  
Gilchrist, B.A., Yaar, M. and Eller, M.  
Use of locally applied dna fragments  
Patent: WO 0174342-A 4 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)

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Best Local Similarity		100.0%; Pred. No. 8.7e+09;					
Matches		5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 CATAC 5						
Db	5 CATAC 1						
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AX268758		AX268758		Sequence 6 from Patent WO0174342.		5 bp DNA	
LOCUS		AX268758		Sequence 6 from Patent WO0174342.		7 bp DNA	
DEFINITION		AX268758		Sequence 6 from Patent WO0174342.			
ACCESSION		AX268758		Sequence 6 from Patent WO0174342.			
VERSION		AX268758.1		GI:16541830			
KEYWORDS							
SOURCE		synthetic construct					
ORGANISM		synthetic construct					
		artificial sequences.					
REFERENCE		1					
AUTHORS		Gilchrest,B.A., Yaar,M. and Eller,M.					
TITLE		Use of locally applied dna fragments					
JOURNAL		Patent: WO 0174342-A 6 11-OCT-2001;					
TRUSTEES		OF BOSTON UNIVERSITY (US)					
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AX268755/c		AX268755		Sequence 3 from Patent WO0174342.		7 bp DNA	
LOCUS		AX268755		Sequence 3 from Patent WO0174342.			
DEFINITION		AX268755		Sequence 3 from Patent WO0174342.			
ACCESSION		AX268755		Sequence 3 from Patent WO0174342.			
VERSION		AX268755.1		GI:16541827			
KEYWORDS							
SOURCE		synthetic construct					
ORGANISM		synthetic construct					
		artificial sequences.					
REFERENCE		1					
AUTHORS		Gilchrest,B.A., Yaar,M. and Eller,M.					
TITLE		Use of locally applied dna fragments					
JOURNAL		Patent: WO 0174342-A 3 11-OCT-2001;					
TRUSTEES		OF BOSTON UNIVERSITY (US)					
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LOCUS		AX268759		Sequence 7 from Patent WO0174342.			
DEFINITION		AX268759		Sequence 7 from Patent WO0174342.			
ACCESSION		AX268759		Sequence 7 from Patent WO0174342.			
VERSION		AX268759.1		GI:16541831			
KEYWORDS							
SOURCE		synthetic construct					
ORGANISM		synthetic construct					
		artificial sequences.					
REFERENCE		1					
AUTHORS		Gilchrest,B.A., Yaar,M. and Eller,M.					
TITLE		Use of locally applied dna fragments					
JOURNAL		Patent: WO 0174342-A 7 11-OCT-2001;					
TRUSTEES		OF BOSTON UNIVERSITY (US)					
FEATURES		Location/Qualifiers					
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Matches		5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 CATAC 5						
Db	2 CATAC 6						

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RESULT 6
AX104946/c
LOCUS AX104946 8 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1138 from Patent WO0122972.
ACCESSION AX104946
VERSION AX104946.1 GI:13921143
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 8)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 1138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
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QY 1 CATAAC 5
Db |||||
7 CATAAC 3

RESULT 7
AX119567/c
LOCUS AX119567 8 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 224 from Patent WO0129251.
ACCESSION AX119567
VERSION AX119567.1 GI:14036486
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Messiaen,L. and Callens,T.
JOURNAL Improved mutation analysis of the nf1 gene
UNIVERSITEIT GENT (BE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Db |||||
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BD085298
LOCUS BD085298 8 bp DNA linear PAT 27-AUG-2002
DEFINITION DNA-based transposon system for the introduction of nucleic acid
into DNA of a cell.
ACCESSION BD085298
VERSION BD085298.1 GI:22630908
KEYWORDS JP 2001523450-A/10.

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 8)
AUTHORS Hackett,P.B., Clark,K.J., Daple,A.J., Ekar,S.C., Larjespayda,D.A.,
Ibycus,Z. and Issufark,T.
TITLE DNA-based transposon system for the introduction of nucleic acid
into DNA of a cell
JOURNAL Patent: JP 2001523450-A 10 27-NOV-2001;
REGENTS OF THE UNIVERSITY OF MINNESOTA
COMMENT OS Artificial Sequence
PN JP 2001523450-A/10
PD 27-NOV-2001
PF 13-NOV-1998 JP 2000521183
PR 13-NOV-1997 US 60/065303
PI PERRY B HACKETT,KARL J CLARK,ADAM J DAPIE,STEVEN C EKAR, PI
DAVID A LARJESPAYDA,ZOLTAN IVCUS,TSSUSANNA ISSUFARK PC
C12N15/09,A01K67/027,C07K16/18,C12N5/10,C12Q1/68,C12N15/00, PC
C12N5/00
CC Description of Artificial Sequence: A portion of a direct CC
repeat sequence
FH Key Location/Qualifiers
FT source 1..8
FT /organism='Artificial Sequence'.
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/mol_type="genomic DNA"
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db |||||
2 CATAAC 6

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BD191357
LOCUS BD191357 8 bp DNA linear PAT 17-JUL-2003
DEFINITION DNA-based transposon system for the introduction of nucleic acid
into DNA of a cell.
ACCESSION BD191357
VERSION BD191357.1 GI:33001096
KEYWORDS JP 2002511741-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 8)
AUTHORS Hackett,P.B., Ivics,Z., Izsvak,Z. and Caldovic,L.
TITLE DNA-based transposon system for the introduction of nucleic acid
into DNA of a cell
JOURNAL Patent: JP 2002511741-A 10 16-APR-2002;
REGENTS OF THE UNIV OF MINNESOTA
COMMENT PN JP 2002511741-A/10
PD 16-APR-2002
PF 11-MAR-1998 JP 1998539720
PI PERRY B HACKETT,ZOLTAN IVCIS,ZSUZSANNA IZSVAK,LJUBICA CALDOVIC
PC C12N15/90,C12N5/16,A01K67/027,C07K16/18
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CC Topology: Linear;
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Best Local Similarity 100.0%; Pred. No. 5.4e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
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Db 2 CATAC 6

RESULT 10  
AX268753/c  
LOCUS AX268753 9 bp DNA linear PAT 29-OCT-2001  
DEFINITION Sequence 1 from Patent WO0174342.  
ACCESSION AX268753  
VERSION AX268753.1 GI:16541825  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Gilchrist,B.A., Yaar,M. and Eller,M.  
TITLE Use of locally applied dna fragments  
JOURNAL Patent: WO 0174342-A 1 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)

FEATURES  
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ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
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Db 7 CATAC 3

RESULT 11  
AX667174  
LOCUS AX667174 9 bp DNA linear PAT 26-MAR-2003  
DEFINITION Sequence 623 from Patent WO0242459.  
ACCESSION AX667174  
VERSION AX667174.1 GI:29291326  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Liu,Q.  
TITLE Position dependent recognition of gnn nucleotide triplets by zinc  
fingers  
JOURNAL Patent: WO 0242459-A 623 30-MAY-2002;  
Sangamo Biosciences Inc. (US)

FEATURES  
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ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
|||||  
Db 2 CATAC 6

RESULT 12  
AX668771/c  
LOCUS AX668771 9 bp DNA linear PAT 26-MAR-2003  
DEFINITION Sequence 2220 from Patent WO0242459.  
ACCESSION AX668771  
VERSION AX668771.1 GI:29291746  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Liu,Q.  
TITLE Position dependent recognition of gnn nucleotide triplets by zinc  
fingers  
JOURNAL Patent: WO 0242459-A 2220 30-MAY-2002;  
Sangamo Biosciences Inc. (US)

FEATURES  
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ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
|||||  
Db 8 CATAC 4

RESULT 13  
AX668807/c  
LOCUS AX668807 9 bp DNA linear PAT 26-MAR-2003  
DEFINITION Sequence 2256 from Patent WO0242459.  
ACCESSION AX668807  
VERSION AX668807.1 GI:29291782  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Liu,Q.  
TITLE Position dependent recognition of gnn nucleotide triplets by zinc  
fingers  
JOURNAL Patent: WO 0242459-A 2256 30-MAY-2002;  
Sangamo Biosciences Inc. (US)

FEATURES  
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ORIGIN

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Qy 1 CATAC 5  
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Db 8 CATAC 4

RESULT 14  
AX805897/c  
LOCUS AX805897 9 bp DNA linear PAT 25-NOV-2003  
DEFINITION Sequence 43 from Patent WO03060163.  
ACCESSION AX805897  
VERSION AX805897.1 GI:38522808  
KEYWORDS

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     van Eijk,M.J. and van Schaik,C.
TITLE       Discrimination and detection of target nucleotide sequences using
            mass spectrometry
JOURNAL     Patent: WO 03060163-A 43 24-JUL-2003;
            Keygene N.V. (NL)
FEATURES
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QY      1 CATAC 5
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Db      8 CATAC 4

RESULT 15
S50583/c
LOCUS      S50583
DEFINITION type I procollagen [human, mRNA Mutant, 9 nt].
ACCESSION  S50583
VERSION    S50583.1 GI:233928
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 9)
AUTHORS     Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.
TITLE       Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
            type I procollagen in lethal osteogenesis imperfecta. The
            conformational strain on the triple helix introduced by a glycine
            substitution can be transmitted along the helix
JOURNAL     J. Biol. Chem. 266 (24), 15608-15613 (1991)
MEDLINE    91340689
PUBMED     1874719
REMARK     GenBank staff at the National Library of Medicine created this
            entry [NCBI gbbseq 50583] from the original journal article.
            This sequence comes from Fig 5A.
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gene

ORIGIN

Query Match      100.0%; Score 5; DB 9; Length 9;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
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Db      9 CATAC 5

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
293.960 Million cell updates/sec

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Perfect score: 5  
Sequence: 1 catcac 5

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Maximum DB seq length: 200

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	AAZ10696	Aaz10696 Oligonucleotide
2	5	100.0	5	AAZ10695	Aaz10695 Oligonucleotide
3	5	100.0	5	AAZ14910	Aasi4910 Melanogen
4	5	100.0	5	AAZ14908	Aasi4908 Melanogen
5	5	100.0	5	ACD25823	Telomere-ACD25823
6	5	100.0	5	ACD25825	Telomere-ACD25825
7	5	100.0	6	ACA88955	Selection ACA88955
8	5	100.0	7	AAZ10694	Aaz10694 Oligonucleotide
9	5	100.0	7	AAZ14911	Aasi4911 Melanogen
10	5	100.0	7	AAZ14907	Aasi4907 Melanogen
11	5	100.0	7	ACD25826	Melanogen ACD25826
12	5	100.0	7	ACD25822	Telomere-ACD25822
13	5	100.0	8	AAZ02250	Direct repeat AAZ02250
14	5	100.0	9	AAZ15899	Aavi5899 Cyclin D
15	5	100.0	9	AAV22350	A promote AAV22350
16	5	100.0	9	AAV22283	GAS complex AAV22283
17	5	100.0	9	AAZ10692	Oligonucleotide AAZ10692
18	5	100.0	9	AAZ14905	Melanogen AAZ14905
19	5	100.0	9	ABQ71504	Zinc finger ABQ71504
20	5	100.0	9	ABQ71958	Zinc finger ABQ71958
21	5	100.0	9	ABQ71922	Zinc finger ABQ71922
22	5	100.0	9	ABX03786	Human DNA ABX03786
23	5	100.0	9	ACD25820	Telomere-ACD25820

## ALIGNMENTS

## RESULT 1

AAZ10696  
ID AAZ10696 standard; DNA; 5 BP.  
XX  
AC AAZ10696;  
XX  
DT 23-NOV-1999 (first entry)  
XX  
DE Oligonucleotide sequence that increases p53 activity in a cell.  
XX  
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
KW skin cancer; ss.  
OS Synthetic.  
XX  
FN GB2336157-A.  
XX  
PD 13-OCT-1999.  
XX  
PF 24-MAR-1999; 99GB-00006758.  
XX  
PR 26-MAR-1998; 98US-00048927.  
XX  
(UYBO-) UNIV BOSTON.  
XX  
GI Gilchrist BA, Yaar M, Eller M;  
XX  
WI WPI; 1999-543520/46.  
XX  
PT DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases.  
XX  
PS Claim 11; Page 30; 44pp; English.  
XX  
CC AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer  
XX  
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

C 24 5 100.0 9 8 ADA64249  
25 5 100.0 9 8 ADA62652  
c 26 5 100.0 9 8 ADA64285  
27 5 100.0 10 2 AAQ43164  
c 28 5 100.0 10 2 AAQ71104  
29 5 100.0 10 2 AAX32625  
c 30 5 100.0 10 2 AAQ97224  
c 31 5 100.0 10 2 AAT35734  
32 5 100.0 10 2 AAT66073  
c 33 5 100.0 10 2 AAV50250  
c 34 5 100.0 10 2 AAV50271  
35 5 100.0 10 2 AAV50127  
36 5 100.0 10 2 AAV50184  
c 37 5 100.0 10 2 AAV35934  
c 38 5 100.0 10 2 AAV35910  
c 39 5 100.0 10 2 AAX18629  
40 5 100.0 10 2 AAV73806  
c 41 5 100.0 10 2 AAZ78624  
c 42 5 100.0 10 3 AAZ79270  
43 5 100.0 10 3 AAZ77574  
44 5 100.0 10 3 AAZ78121  
c 45 5 100.0 10 3 AAZ78625

Ada64249 Zinc finger  
Ada62652 Zinc finger  
Ada64285 Zinc finger  
Aaq43164 Donor oli  
Aaq71104 Merlin ex  
Aax32625 Anticancer  
Aaq97224 Oligonucle  
Aat35734 Primer E1  
Aat66073 (dc-da)n.  
Aav50250 Yeast tag  
Aav50271 Yeast tag  
Aav50127 Yeast tag  
Aav50184 Yeast tag  
Aav35934 Primer us  
Aav35910 Primer us  
Aax18629 p53 seria  
Aav73806 Chromoph  
Aaz78624 Human den  
Aaz79270 Human den  
Aaz77574 Human den  
Aaz78121 Human den  
Aaz78625 Human den

Query Match 100.0%; Score 5; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+08; Indels 0;  
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATAC 5  
 |||||  
 Db 1 CATAC 5

RESULT 2  
 AAZ10695/c  
 ID AAZ10695 standard; DNA; 5 BP.  
 XX  
 AC AAZ10695;  
 XX  
 DT 23-NOV-1999 (first entry)  
 XX  
 DE Oligonucleotide sequence that increases p53 activity in a cell.  
 XX  
 KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 KW skin cancer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN GB2336157-A.  
 XX  
 PD 13-OCT-1999.  
 XX  
 PF 24-MAR-1999; 99GB-00006759.  
 XX  
 PR 26-MAR-1998; 98US-00048927.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 XX  
 PI Gilchrist BA, Yaar M, Eller M;  
 XX  
 DR WPI; 1999-543520/46.  
 XX  
 DN DNA fragments useful for increasing p53 activity in a cell and reducing  
 susceptibility to UV-induced hyperproliferative diseases.  
 PT  
 PS Claim 11; Page 30; 44pp; English.  
 XX  
 CC AAZ10692-97 represent DNA fragments that are used for increasing p53  
 activity in a cell. The oligonucleotides are UV mimetics and protect  
 cells against subsequent exposure to UV-irradiation or chemicals. The  
 CC oligonucleotides are useful for increasing p53 activity in a cell,  
 CC reducing the susceptibility to UV-induced hyperproliferative diseases,  
 CC treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,  
 CC conjunctivitis, and UV-induced dermatoses, reducing photoaging and  
 CC reducing susceptibility to skin cancer  
 XX  
 SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 |||||  
 Db 5 CATAC 1

RESULT 3  
 AAS14910  
 ID AAS14910 standard; DNA; 5 BP.  
 XX  
 AC AAS14910;  
 XX  
 DT 14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #6.  
 DE  
 XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200174342-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US010162.  
 XX  
 PR 31-MAR-2000; 2000US-00540843.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 XX  
 PI Gilchrist BA, Yaar M, Eller M;  
 XX  
 DR WPI; 2001-626338/72.  
 XX  
 DN Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 carcinoma, using specific oligonucleotides that mimic the effects of  
 ultra-violet light.  
 PT  
 PS Claim 1; Page 36; 74pp; English.  
 XX  
 CC The invention describes inhibition of mammalian epithelial cell  
 proliferation by treating cells with at least one oligonucleotide, or its  
 CC fragment. The compounds, which have cytostatic, anti-allergic, anti-  
 CC inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to: treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergically mediated inflammation (atopic or contact dermatitis,  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #6, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,  
 CC described in the method of the invention  
 XX  
 SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 |||||  
 Db 1 CATAC 5

RESULT 4  
 AAS14908/c  
 ID AAS14908 standard; DNA; 5 BP.  
 XX  
 AC AAS14908;



CC pigmentosum, seborrhic keratosis, actinic keratosis, Bowen's disease, or  
 CC basal cell carcinoma) and for treating or preventing pre-cancerous  
 CC conditions affecting epithelial cells (such as psoriasis and atopic  
 CC dermatitis) and also the types of cancers of breast, lung, liver,  
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,  
 CC oesophagus, stomach, and thyroid. The present sequence is a truncated  
 CC telomere-like oligonucleotide of the invention  
 XX  
 SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CATAC 5  
 Db 5 CATAC 1  
 RESULT 6  
 ACD25825  
 ID ACD25825 standard; DNA; 5 BP.  
 XX AC ACD25825;  
 XX  
 DT 08-SEP-2003 (first entry)  
 XX  
 DE Telomere-like oligonucleotide #3.  
 XX  
 KW Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological;  
 KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;  
 KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;  
 KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;  
 KW gp-1100; hyperproliferative disorder; spongiosis; blistering;  
 KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrhic keratosis;  
 KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;  
 KW atopic dermatitis; breast cancer; lung cancer; liver cancer;  
 KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;  
 KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;  
 KW stomach cancer; thyroid cancer.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "5, phosphorylated"  
 XX  
 XX US2003032610-A1.  
 XX  
 PD 13-FEB-2003.  
 XX  
 XX 12-APR-2002; 2002US-00122630.  
 XX  
 PR 03-JUN-1996; 96WO-US008386.  
 PR 26-MAR-1998; 98US-00048927.  
 PR 31-MAR-2000; 2000US-00540843.  
 PR 30-MAR-2001; 2001WO-US010162.  
 XX  
 XX (GILC/) GILCREST B A.  
 PA (ELLE/) ELLER M S.  
 PA (YAAR/) YAAR M.  
 XX  
 XX Gilchrest BA, Eller MS, Yaar M;  
 PI  
 XX WPI; 2003-512221/48.  
 DR  
 XX  
 XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,  
 PT by administering composition having oligonucleotides that share sequence  
 PT identity with human telomere overhang repeat.  
 XX

PS Claim 44; Page 3; 65pp; English.  
 XX  
 CC The invention relates to inhibiting growth of cancer cells, which is  
 CC independent of presence or activity of telomerase in cells, not requiring  
 CC the presence or activity of p53 normal function in cells, or resulting in  
 CC S-phase arrest in cells, and inducing apoptosis in cancer cells,  
 CC involving administering a composition comprising oligonucleotides which  
 CC share at least 50% sequence identity with human telomere overhang repeat,  
 CC (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their  
 CC contiguous portion) and is used in a method inhibiting proliferation of  
 CC epithelial cells in a mammal or preventing/reducing DNA damage in cells  
 CC of a mammal, where the DNA damage is caused by radiation or DNA-damaging  
 CC chemicals. The method is useful for inhibiting growth of cancer cells  
 CC (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,  
 CC squamous cell carcinoma), for inducing apoptosis in cancer cells in  
 CC human, promoting differentiation of malignant cells in a mammal,  
 CC enhancing the expression of one or more surface antigens (e.g. MART-1,  
 CC tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer  
 CC cells (especially melanoma cells) in a human and for treatment of other  
 CC hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis  
 CC in the skin of a mammal, skin cancer in a human with xeroderma  
 CC pigmentosum, seborrhic keratosis, actinic keratosis, Bowen's disease, or  
 CC basal cell carcinoma) and for treating or preventing pre-cancerous  
 CC conditions affecting epithelial cells (such as psoriasis and atopic  
 CC dermatitis) and also the types of cancers of breast, lung, liver,  
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,  
 CC oesophagus, stomach, and thyroid. The present sequence is a telomere-like  
 CC oligonucleotide of the invention  
 XX  
 SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CATAC 5  
 Db 1 CATAC 5  
 RESULT 7  
 ACA88955/c  
 ID ACA88955 standard; DNA; 6 BP.  
 XX AC ACA88955;  
 XX  
 DT 08-JUL-2003 (first entry)  
 DE  
 XX Selection and amplification of genetic markers PCR related primer #66.  
 XX  
 KW Genetic marker selection; multiplex PCR amplification;  
 KW prenatal diagnostic testing; foetal sex determination;  
 KW genetic identification; DNA profiling; DNA fingerprinting;  
 KW forensic analysis; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003031646-A1.  
 XX  
 PD 17-APR-2003.  
 XX  
 XX 14-OCT-2002; 2002WO-AU001388.  
 XX  
 XX 12-OCT-2001; 2001AU-00008234.  
 PR  
 PR 12-OCT-2001; 2001AU-00008235.  
 XX  
 XX (UYQU ) UNIV QUEENSLAND.  
 PA  
 XX Findlay I, Matthews PL, Mulcahy BK;  
 PI  
 XX WPI; 2003-381725/36.  
 DR  
 XX Selecting genetic markers as targets for nucleic acid sequence  
 PT

PT amplification, useful for improving genetic testing, e.g. fetal sex  
 PT determination, comprises selecting each of the genetic markers according  
 PT to a heterozygosity index.

XX Claim 36; Page 40; 64pp; English.

XX The invention describes a method of selecting genetic markers as targets  
 CC for nucleic acid sequence amplification comprising selecting each of the  
 CC genetic markers according to a heterozygosity index of 0.5 or greater.  
 CC Selecting and amplification of genetic markers are useful as targets for  
 CC nucleic acid sequence amplification, for genetic testing or facilitating  
 CC multiplex PCR amplification from limiting amounts of target nucleic acid.  
 CC The methods are also useful for improving genetic diagnostic and  
 CC screening methods, such as prenatal diagnostic testing, foetal sex  
 CC determination or genetic identification, e.g. DNA profiling or DNA  
 CC fingerprinting. The nucleic acid sequence amplification is also useful in  
 CC forensic analysis of degraded, old, ancient and difficult samples that  
 CC are difficult to amplify and identify. This sequence represents a PCR  
 CC primer used in the selection and amplification of genetic markers

XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 7; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
 Db |||||  
 6 CATAC 2

RESULT 8

AAZ10694/C  
 ID AAZ10694 standard; DNA; 7 BP.

XX AC AAZ10694;

XX DT 23-NOV-1999 (first entry)

XX DE Oligonucleotide sequence that increases p53 activity in a cell.

XX KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 KW skin cancer; ss.

XX OS Synthetic.

XX PN GB2336157-A.

XX PD 13-OCT-1999.

XX PF 24-MAR-1999; 99GB-00006758.

XX PR 26-MAR-1998; 98US-00048927.

XX PA (UYBO-) UNIV BOSTON.

XX PI Gilchrist BA, Yaar M, Eller M;

XX PS WPI; 1999-543520/46.

XX PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases.

XX PS Claim 11; Page 30; 44pp; English.

XX CC AAZ10692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are used for increasing p53  
 CC cells against subsequent exposure to UV-irradiation or chemicals. The  
 CC oligonucleotides are useful for increasing p53 activity in a cell,  
 CC reducing the susceptibility to UV-induced hyperproliferative diseases,  
 CC treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,

CC conjunctivitis, and UV-induced dermatoses, reducing photoaging and  
 CC reducing susceptibility to skin cancer

XX SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
 Db |||||  
 6 CATAC 2

RESULT 9

AAS14911/C

ID AAS14911 standard; DNA; 7 BP.

XX AC AAS14911;

XX DT 14-FEB-2002 (first entry)

XX DE Melanogenesis associated oligonucleotide #7.

XX KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.

XX OS Synthetic.

XX PH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= a  
 FT /note= "Phosphorylated"

XX PN WO200174342-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US010162.

XX PR 31-MAR-2000; 2000US-00540843.

XX PA (UYBO-) UNIV BOSTON.

XX PI Gilchrist BA, Yaar M, Eller M;

XX PS WPI; 2001-626338/72.

XX PT Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 PT carcinoma, using specific oligonucleotides that mimic the effects of  
 PT ultra-violet light.

XX PS Claim 1; Page 38; 74pp; English.

XX CC The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or its  
 CC fragment. The compounds, which have cytostatic, anti-allergic, anti-  
 CC inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat

CC allergically mediated inflammation (atopic or contact dermatitis,  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #7, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,  
 CC described in the method of the invention

SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 Db 6 CATAC 2  
 |||||  
 |||||

RESULT 10  
 AAS14907/c  
 ID AAS14907 standard; DNA; 7 BP.  
 XX AAS14907;  
 AC AAS14907;  
 DT 14-FEB-2002 (first entry)  
 DE Melanogenesis associated oligonucleotide #3.  
 DE Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
 XX Synthetic.  
 OS  
 XX WO200174342-A2.  
 PN  
 XX 11-OCT-2001.  
 PD  
 XX 30-MAR-2001; 2001WO-US010162.  
 PF  
 XX 31-MAR-2000; 2000US-00540843.  
 PR (UYBO-) UNIV BOSTON.  
 PA  
 XX Gilchrist BA, Yaar M, Eller M;  
 PI WPI; 2001-626338/72.  
 DR  
 XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 PT carcinoma, using specific oligonucleotides that mimic the effects of  
 PT ultra-violet light.  
 XX  
 XX Claim 1; Page 36; 74pp; English.  
 XX  
 CC The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or its  
 CC fragment. The compounds, which have cytostatic, anti-allergic, anti-  
 CC inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to: treat

CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergically mediated inflammation (atopic or contact dermatitis,  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #3, a truncated  
 CC version of the oligonucleotide shown in AAS14906, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,  
 CC described in the method of the invention

SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 Db 6 CATAC 2  
 |||||  
 |||||

RESULT 11  
 ACD25826/c  
 ID ACD25826 standard; DNA; 7 BP.  
 XX ACD25826;  
 AC ACD25826;  
 DT 08-SEP-2003 (first entry)  
 DE Melanogenic telomere-like oligonucleotide #1.  
 DE Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological;  
 KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;  
 KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;  
 KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;  
 KW gp-1100; hyperproliferative disorder; spongiolysis; blistering;  
 KW dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis;  
 KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;  
 KW atopic dermatitis; breast cancer; lung cancer; liver cancer;  
 KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;  
 KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;  
 KW stomach cancer; thyroid cancer.  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= '5' phosphorylated"  
 FT  
 XX US2003032610-A1.  
 PN  
 XX 13-FEB-2003.  
 PD  
 XX 12-APR-2002; 2002US-00122630.  
 PF  
 XX 03-JUN-1996; 96WO-US008386.  
 PR 26-MAR-1998; 98US-00048927.  
 PR 31-MAR-2000; 2000US-00540843.  
 PR 30-MAR-2001; 2001WO-US010162.  
 XX (GILC/) GILCHREST B A.  
 PA (ELLE/) ELLER M S.  
 PA (YAAR/) YAAR M.  
 XX Gilchrist BA, Eller MS, Yaar M;  
 PI WPI; 2003-512221/48.  
 DR

XX Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,  
 PT by administering composition having oligonucleotides that share sequence  
 PT identity with human telomere overhang repeat.  
 XX  
 PS Claim 44; Page 18; 65pp; English.  
 XX  
 CC The invention relates to inhibiting growth of cancer cells, which is  
 CC independent of presence or activity of telomerase in cells, not requiring in  
 CC the presence or activity of p53 normal function in cells, or resulting in  
 CC S-phase arrest in cells, and inducing apoptosis in cancer cells,  
 CC involving administering a composition comprising oligonucleotides which  
 CC share at least 50% sequence identity with human telomere overhang repeat,  
 CC (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their  
 CC contiguous portion) and is used in a method inhibiting proliferation of  
 CC epithelial cells in a mammal or preventing/reducing DNA damage in cells  
 CC of a mammal, where the DNA damage is caused by radiation or DNA-damaging  
 CC chemicals. The method is useful for inhibiting growth of cancer cells  
 CC (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,  
 CC squamous cell carcinoma), for inducing apoptosis in cancer cells in  
 CC human, promoting differentiation of malignant cells in a mammal,  
 CC enhancing the expression of one or more surface antigens (e.g. MART-1,  
 CC tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer  
 CC cells (especially melanoma cells) in a human and for treatment of other  
 CC hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis  
 CC in the skin of a mammal, skin cancer in a human with xeroderma  
 CC pigmentosum, seboreithic keratosis, actinic keratosis, Bowen's disease, or  
 CC basal cell carcinoma) and for treating or preventing pre-cancerous  
 CC conditions affecting epithelial cells (such as psoriasis and atopic  
 CC dermatitis) and also the types of cancers of breast, lung, liver,  
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,  
 CC oesophagus, stomach, and thyroid. The present sequence is a melanogenic  
 CC telomere-like oligonucleotide of the invention  
 XX  
 SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CATAC 5  
 Db |||||  
 6 CATAC 2  
 RESULT 12  
 ACD25822/c  
 ID ACD25822 standard; DNA; 7 BP.  
 XX  
 AC ACD25822;  
 XX  
 DT 08-SEP-2003 (first entry)  
 XX  
 DE Telomere-like oligonucleotide #1 truncated version #1.  
 XX  
 KW Telomere; ss; probe; cytostatic; human; antiproliferative; dermatological;  
 KW apoptosis; cancer; p53; epithelial cell proliferation; DNA damage;  
 KW lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer;  
 KW squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1;  
 KW gp-1100; hyperproliferative disorder; spongiosis; blistering;  
 KW dyskeratosis; skin cancer; xeroderma pigmentosum; seboreithic keratosis;  
 KW actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis;  
 KW atopic dermatitis; breast cancer; lung cancer; liver cancer;  
 KW prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer;  
 KW uterine cancer; colon cancer; brain cancer; oesophageal cancer;  
 KW stomach cancer; thyroid cancer.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a

FT  
 FT /mod\_base= OTHER  
 XX /note= "5' phosphorylated"  
 PN US2003032610-A1.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 12-APR-2002; 2002US-00122630.  
 XX  
 PR 03-JUN-1996; 96WO-US008386.  
 PR 26-MAR-1998; 98US-00048927.  
 PR 31-MAR-2000; 2000US-00540843.  
 PR 30-MAR-2001; 2001WO-US010162.  
 XX  
 PA (GILC/) GILCHREST B A.  
 PA (ELLE/) ELLER M S.  
 PA (YAAR/) YAAR M.  
 XX  
 PI Gilchrest BA, Eller MS, Yaar M;  
 XX  
 DR WPI; 2003-512221/48.  
 XX  
 PT Inhibiting growth of cancer cells and inducing apoptosis in cancer cells,  
 PT by administering composition having oligonucleotides that share sequence  
 PT identity with human telomere overhang repeat.  
 XX  
 PS Claim 44; Page 6; 65pp; English.  
 XX  
 CC The invention relates to inhibiting growth of cancer cells, which is  
 CC independent of presence or activity of telomerase in cells, not requiring in  
 CC the presence or activity of p53 normal function in cells, or resulting in  
 CC S-phase arrest in cells, and inducing apoptosis in cancer cells,  
 CC involving administering a composition comprising oligonucleotides which  
 CC share at least 50% sequence identity with human telomere overhang repeat,  
 CC (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their  
 CC contiguous portion) and is used in a method inhibiting proliferation of  
 CC epithelial cells in a mammal or preventing/reducing DNA damage in cells  
 CC of a mammal, where the DNA damage is caused by radiation or DNA-damaging  
 CC chemicals. The method is useful for inhibiting growth of cancer cells  
 CC (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer,  
 CC squamous cell carcinoma), for inducing apoptosis in cancer cells in  
 CC human, promoting differentiation of malignant cells in a mammal,  
 CC enhancing the expression of one or more surface antigens (e.g. MART-1,  
 CC tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer  
 CC cells (especially melanoma cells) in a human and for treatment of other  
 CC hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis  
 CC in the skin of a mammal, skin cancer in a human with xeroderma  
 CC pigmentosum, seboreithic keratosis, actinic keratosis, Bowen's disease, or  
 CC basal cell carcinoma) and for treating or preventing pre-cancerous  
 CC conditions affecting epithelial cells (such as psoriasis and atopic  
 CC dermatitis) and also the types of cancers of breast, lung, liver,  
 CC prostate, pancreatic, ovarian, bladder, uterine, colon, brain,  
 CC oesophagus, stomach, and thyroid. The present sequence is a truncated  
 CC telomere-like oligonucleotide of the invention  
 XX  
 SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CATAC 5  
 Db |||||  
 6 CATAC 2  
 RESULT 13  
 AAD02250  
 ID AAD02250 standard; DNA; 8 BP.  
 XX  
 AC AAD02250;  
 XX  
 DT 28-MAR-2001 (first entry)

XX DE Direct repeat sequence that binds to SB protein.  
 XX KW Sleeping Beauty; SB; AdSB10; adenovirus; transposase;  
 KW non-integrating viral vector; cytostatic; anti-diabetic; cardiant;  
 KW neuroprotective; genetic disease; gene therapy; therapy; cancer;  
 KW cystic fibrosis; diabetes; cardiovascular disease; brain malfunction;  
 KW genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.  
 XX OS Unidentified.  
 XX OS WO200068399-A2.  
 XX PN 16-NOV-2000.  
 XX PD  
 XX PF 11-MAY-2000; 2000WO-US012827.  
 XX PR 11-MAY-1999; 99US-0133569P.  
 XX PA (MINU ) UNIV MINNESOTA.  
 XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 XX PA (MCIV/) MCIVOR R S.  
 XX PA (HACK/) HACKETT P B.  
 XX PA (AGUI/) AGUILAR-CORDOVA E.  
 XX PI Mcivor RS, Hackett PB, Aguilar-Cordova E;  
 XX DR WPI; 2001-024870/03.  
 XX PT Non-integrating (adenovirus-based) viral vectors useful in gene therapy,  
 XX PT especially for treating patients suffering from a genetic disease, e.g.  
 XX PT cystic fibrosis, diabetes, cardiovascular disease, cancer or brain  
 XX PT malfunction.  
 XX PS Disclosure; Page 14; 62pp; English.  
 XX CC The patent discloses non-integrating viral vectors comprising a  
 CC polynucleotide flanked by inverted repeats that bind a transposase, a  
 CC transposase-encoding polynucleotide operably linked to a regulatory  
 CC sequence comprising an operator, that alters expression of the  
 CC transposase-encoding polynucleotide. Transposon sequences can integrate  
 CC into genomic DNA whether or not the cell is dividing. AdSB10 is a SB  
 CC (Sleeping Beauty) transposase-transducing adenoviral non-integrating  
 CC vector. The non-integrating viral vectors are useful for treating genetic  
 CC disease characterised by subnormal production of a polypeptide or RNA,  
 CC e.g. for replacement of a defective gene, delivery of a polypeptide drug  
 CC or supplementation of a metabolic activity. These genetic diseases  
 CC include cystic fibrosis, diabetes, cardiovascular disease, cancer or  
 CC brain malfunction. The non-integrating viral vectors are useful as  
 CC nucleic acid delivery systems, e.g. for genome analysis or gene therapy  
 CC and can also be used for applications that involve long-term production  
 CC of a polypeptide. The non-integrating viral vectors are also useful for  
 CC creating transgenic host cells that provide normal cells with protection  
 CC against toxic side effects of chemotherapy. The sequence of the present  
 CC invention is a direct repeat sequence that binds to SB protein  
 XX SQ Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CATAC 5  
 Db |||||  
 2 CATAC 6  
 RESULT 14  
 AAV15899/c  
 ID AAV15899 standard; DNA; 9 BP.  
 XX AAV15899;  
 AC  
 XX

DT 26-MAY-1998 (first entry)  
 XX Cyclin D transcription factor DMP1 nonamer consensus sequence.  
 XX KW cyclin D transcription factor; binding affinity; D-type cyclin; probe;  
 KW cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;  
 KW nonamer consensus sequence; ss.  
 XX OS Mus musculus.  
 XX OS Homo sapiens.  
 XX PN WO9743415-A1.  
 XX XX 20-NOV-1997.  
 XX PF 16-MAY-1997; 97WO-US008480.  
 XX PR 16-MAY-1996; 96US-0017815P.  
 XX PR 16-MAY-1996; 96US-00648837.  
 XX PR 15-MAY-1997; 97US-00257071.  
 XX PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
 XX XX Hirai H, Sherr CJ, Inoue K;  
 XX WPI; 1998-008884/01.  
 XX CC Cyclin D transcription factor and related DNA - can be used to develop  
 XX CC products for treatment of, e.g. cancer.  
 XX PS Claim 3; Page 99; 120pp; English.  
 XX CC This is a nonamer consensus sequence of a cyclin D transcription factor  
 CC DMP1. DMP1 is an amino acid polymer which has binding affinity for a D-  
 CC type cyclin, in vitro, and for a specific DNA nucleotide sequence and is  
 CC a transcription factor involved in the activation of genes that prevent  
 CC cell proliferation. The DMP1 nucleic acid is operatively linked to an  
 CC expression control sequence in an expression vector. The expression  
 CC vector has a transcription control sequence comprising this nonamer  
 CC sequence operably associated with a recombinant gene or a cassette  
 CC insertion site for a recombinant gene. The vector is homologously  
 CC recombined in a chromosome of a transgenic animal. A probe or a  
 CC competitor in DMP1 transactivation assays is designed based on this  
 CC nonamer sequence. The presence of activity of DMP1 can be determined by  
 CC detecting binding of DMP1 and a probe by contacting a biological sample  
 CC from a mammal with the probe under conditions that allow binding of the  
 CC probe to DMP1, where the probe contains the core sequence GTA, and where  
 CC the presence or activity of DMP1 is suspected in the sample. DMP1 can  
 CC function as a cell cycle inhibitor when expressed in a tumour cell.  
 CC Modulating the expression of DMP1 can be used to treat tumours and other  
 CC cancers. DMP1 can also be used for controlling expression of heterologous  
 CC proteins. Antisense sequences and ribozymes can be used to inhibit  
 CC expression of the transcription factor. Detecting the level and activity  
 CC of DMP1 in cells is useful for detection of cancer cells or  
 CC dysproliferative cells  
 XX SQ Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CATAC 5  
 Db |||||  
 8 CATAC 4  
 RESULT 15  
 AAV22350/c  
 ID AAV22350 standard; RNA; 9 BP.  
 XX  
 AC AAV22350;  
 XX

DT 29-JUN-1998 (first entry)  
 XX  
 DE A promoter regulatory motif found in the utrons of the invention.  
 XX  
 KW 3' untranslated region; UTR; inhibition; gene expression; ICAM-7;  
 KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;  
 KW antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;  
 KW HIV gene expression; transplant rejection; treatment; autoimmune disease;  
 KW inflammatory disease; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX WO9744450-A1.  
 PN  
 XX  
 XX 27-NOV-1997.  
 PD  
 XX  
 XX 21-MAY-1997; 97WO-US009459.  
 PF  
 XX  
 XX 21-MAY-1996; 96US-00646789.  
 PR  
 XX  
 XX (UYVA ) UNIV YALE.  
 PA  
 XX  
 XX Peyman JA;  
 PI  
 XX  
 XX WPI; 1998-018505/02.  
 DR  
 XX  
 XX Utrons, RNA molecules containing promoter regulatory motifs - useful to  
 PT suppress express expression from promoter of interest, specifically TSU  
 PT nucleic acid suppression of MHC Class I and II gene expression.  
 XX  
 XX Claim 20; Page 20; 200pp; English.  
 PS  
 XX  
 XX The present sequence represents a promoter regulatory element, found in  
 CC the utrons of the invention. Utrons are from, or are homologous to, the  
 CC 3' untranslated region (UTR), of an mRNA that stimulates or inhibits a  
 CC cellular response by sequence specific interactions. The utron is able to  
 CC suppress constitutive and interferon-gamma (IFN-gamma) induced major  
 CC histocompatibility complex (MHC) class I and class II antigen expression  
 CC and expression of other antigens, the gene promoters of which contain  
 CC related sequence motifs that are stimulated by the same factors which  
 CC stimulate MHC class I and class II antigen expression. Such utrons can be  
 CC used to regulate gene expression in a subject, e.g. a human or a cell in  
 CC vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7-1, B7-2, Fc  
 CC gamma R, IL-2 or HIV gene expression. They can be used to inhibit  
 CC transplant rejection, or treat an autoimmune or inflammatory disease or  
 CC disorder  
 XX  
 SQ Sequence 9 BP; 3 A; 0 C; 3 G; 0 T; 3 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CATAC 5  
 Db 5 CATAC 1

Search completed: August 11, 2004, 17:56:32  
 Job time : 76.5914 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 16:50:49 ; Search time 598.548 Seconds  
(without alignments)  
249.455 Million cell updates/sec

Title: US-09-540-843-6  
Perfect score: 5  
Sequence: 1 catac 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0  
Maximum DB seq length: 200

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estm:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estl:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est4:\*

13: gb\_est5:\*

14: gb\_estfun:\*

15: em\_estcom:\*

16: em\_gss\_hum:\*

17: em\_gss\_inv:\*

18: em\_gss\_pln:\*

19: em\_gss\_vrt:\*

20: em\_gss\_fun:\*

21: em\_gss\_mam:\*

22: em\_gss\_mus:\*

23: em\_gss\_pro:\*

24: em\_gss\_rod:\*

25: em\_gss\_phg:\*

26: em\_gss\_vxl:\*

27: gb\_gss1:\*

28: gb\_gss2:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	13	14	CF543283
2	5	100.0	14	12	BM398220
3	5	100.0	16	9	AI424037
4	5	100.0	16	9	AI685758

## RESULT 1

CF543283

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CF543283

S014680-024-030-D02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone

024-030-D02 5-PRIME, mRNA sequence.

CF543283

EST.

CF543283.1 GI:34891723

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 13)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radeilof, J.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

## ALIGNMENTS

13 bp mRNA linear EST 22-SEP-2003  
S014680-024-030-D02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-030-D02 5-PRIME, mRNA sequence.

5 100.0 16 9 AI721735  
6 100.0 16 12 BG928185  
7 100.0 17 12 BG929060  
8 100.0 17 13 BG959683  
9 100.0 17 13 C21103  
10 100.0 18 12 BM397954  
11 100.0 19 9 AA977115  
12 100.0 19 9 AI120725  
13 100.0 19 9 AI747751  
14 100.0 19 13 BX551013  
15 100.0 19 13 C00646  
16 100.0 19 28 AZ341880  
17 100.0 19 28 AZ345849  
18 100.0 19 28 AZ355195  
19 100.0 19 28 AZ406137  
20 100.0 19 28 AZ422163  
21 100.0 19 28 AZ434551  
22 100.0 19 28 AZ464990  
23 100.0 19 28 AZ486152  
24 100.0 19 28 AZ579566  
25 100.0 19 28 AZ614702  
26 100.0 19 28 AZ626685  
27 100.0 19 28 AZ645469  
28 100.0 19 28 AZ647364  
29 100.0 19 28 AZ759906  
30 100.0 19 28 AZ766086  
31 100.0 19 28 AZ799396  
32 100.0 19 28 AZ815067  
33 100.0 19 28 AZ817238  
34 100.0 19 28 AZ839614  
35 100.0 19 28 AZ864822  
36 100.0 19 28 AZ942806  
37 100.0 19 28 AZ948421  
38 100.0 19 28 AZ949895  
39 100.0 19 28 AZ953217  
40 100.0 19 28 AZ987324  
41 100.0 19 28 AZ990856  
42 100.0 20 9 AB088508  
43 100.0 20 13 BQ593049  
44 100.0 20 28 AZ336039  
45 100.0 20 28 AZ359199

AI721735 fc31g08.x  
BG928185 HNC65-1-D  
BG929060 HNC11-1-G  
BG959683 E012692-0  
C21103 HUMGS000262  
BM397954 5009-0-39  
AA977115 oq24c08.s  
AI120725 ub72b11.r  
AI747751 ul21h05.x  
BX551013 BX551013  
C00646 HUMGS000819  
AZ341880 IM0074004  
AZ345849 IM0080216  
AZ355195 IM0094G22  
AZ406137 IM0175F16  
AZ422163 IM0200B22  
AZ434551 IM0221C12  
AZ464990 IM0274G11  
AZ486152 IM0314A04  
AZ579566 IM0367L08  
AZ614702 IM0443F10  
AZ626685 IM0467M01  
AZ645469 IM0510L24  
AZ647364 IM0513O16  
AZ759906 IM0553C10  
AZ766086 IM0563G19  
AZ799396 IM0056N18  
AZ815067 IM0083P01  
AZ817238 IM0086E01  
AZ839614 IM0135N16  
AZ864822 IM0174C08  
AZ942806 IM0203F09  
AZ948421 IM0211A01  
AZ949895 IM0213N08  
AZ953217 IM0218A23  
AZ987324 IM0269B21  
AZ990856 IM0274F14  
AB088508 AB088508  
BQ593049 E012375-0  
AZ336039 IM0066E09  
AZ359199 IM0101M19

Email: weissaa@piz-koeln.mpg.de  
 Insert Length: 13 Std Error: 0.00  
 Plate: 30 row: D column: 02  
 Seq primer: SP6.

## FEATURES

source

1. 13  
 Location/Qualifiers  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:936477"  
 /clone="024-030-D02"  
 /tissue\_type="leaf"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MPIZ-ADIS-024-leaf"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator; Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 14; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5

Db 6 CATAC 10

## RESULT 2

BM398220

LOCUS

DEFINITION

5009-0-42-D11.t.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM398220

VERSION

BM398220.1

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila

ORGANISM

Tetrahymena thermophila

REFERENCE

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,

Frankel, J., and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

CONTACT: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1. 14

/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

/strain="CU428.1"

/db\_xref="taxon:5911"

/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 100.0%; Score 5; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5

Db 1 CATAC 5

## RESULT 3

AI424037

LOCUS

DEFINITION

tf51h06.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2102843

similar to TR:Q69566 Q69566 ; mRNA sequence.

ACCESSION

AI424037

VERSION

AI424037.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 16)

AUTHORS

NCI/NINDS-CGAP NCI

TITLE

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/STGAP), Tumor Gene Index

UNPUBLISHED (1998)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonardo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2102843"

/tissue\_type="glioblastoma (pooled)"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Brn23"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCATCTGAAGTGGAGCGCCGATATCTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonardo."

## ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5

Db 2 CATAC 6

## RESULT 4

AI685758  
LOCUS  
DEFINITION  
t137909.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2253280 3'  
Similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL  
SEQUENCE MOTIF PROTEIN 1 ; contains element LTR4 repetitive element  
; mRNA sequence.  
ACCESSION  
AI685758  
VERSION  
AI685758.1 GI:4897052  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
[www-bio.linnl.gov/bbrp/image/image.html](http://www-bio.linnl.gov/bbrp/image/image.html)  
Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
FEATURES  
source  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2253280"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pr28"  
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)  
with a modified polylinker; Plasmid DNA from the  
normalized library NCI CGAP Pr22 was prepared, and ss  
circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneIDs  
985608-986759, 1101192-1101959, and 1217928-1220615).  
Subtraction by Bento Soares and M. Fatima Bonaldo. "  
ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATAC 5  
|||||  
Db 5 CATAC 9  
RESULT 5  
AI721735  
LOCUS  
DEFINITION  
t31908.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone  
IMAGE:3723038 3', similar to SW:YM14\_PARTE P15615 HYPOTHETICAL 47.2  
KD PROTEIN ; mRNA sequence.  
ACCESSION  
AI721735  
VERSION  
AI721735.1 GI:5040064  
KEYWORDS  
EST.  
SOURCE  
Danio rerio (zebrafish)  
ORGANISM  
Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,  
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,  
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
WashU Zebrafish EST Project 1998  
Contact: Stephen L. Johnson  
Other\_ESTs: fc31908.y1  
Unpublished (1998)  
JOURNAL  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [zbrafish@watson.wustl.edu](mailto:zbrafish@watson.wustl.edu)  
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:  
Matthew Clark. DNA Sequencing by: Washington University Genome  
Sequencing Center Clone distribution: Genome Systems, St. Louis,  
Missouri (web address: [www.genomesystems.com](http://www.genomesystems.com)) (email contact:  
[info@genomesystems.com](mailto:info@genomesystems.com)) and Research Genetics, Huntsville, Alabama  
(web address: [www.resgen.com](http://www.resgen.com)) (email contact: [info@resgen.com](mailto:info@resgen.com)) and  
ReSourceGenZentrumPrimaDatenbank, Berlin, Germany (web address:  
[www.rzpd.de](http://www.rzpd.de))  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: T7 ET from Amersham  
High quality sequence stop: 1.  
FEATURES  
source  
1. .16  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:3723038"  
/sex="mixed"  
/tissue\_type="26 somite embryos, adult livers, shield  
stage embryos"  
/lab\_host="XL1-blue MRF"  
/clone\_lib="Zebrafish WashU MPIMG EST"  
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st  
strand cDNA was primed with a Not I - oligo(dT)15 primer  
[5'pgactagttctagatccgagccgcgcctttttttttt3'];  
double-stranded cDNA was ligated to Sal I adaptors (BRL),  
digested with Not I and cloned into the Not I and Sal I  
sites of the pSPORT1 vector (BRL). Library was constructed  
by Matthew Clark (Lehrach lab) ICRF, London and Max Planck  
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST  
analysis were selected following oligonucleotide  
hybridization fingerprinting of arrayed clones from  
zebrafish late somitogenesis (26 ss), adult liver or  
embryonic shield stage (5.6 h) libraries. Fingerprint  
data were used to computationally cluster cDNAs, and a  
single cDNA from each cluster was chosen for sequencing.  
In some cases multiple members of the same cluster were  
sequenced to assess clustering parameters or single clones  
were sequenced additional times to assess quality  
control."  
ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CATAC 5  
|||||  
Db 9 CATAC 13  
RESULT 6  
BG928185

LOCUS BG928185 16 bp mRNA linear EST 06-NOV-2001  
 DEFINITION HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BG928185  
 VERSION BG928185.1 GI:14322708  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.  
 TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
 JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 UW2109

GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay\_kumar-1@gsk.com  
 Seq primer: T7.

FEATURES  
 source  
 1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI; Directional"

ORIGIN  
 Query Match 100.0%; Score 5; DB 12; Length 16;  
 Best Local Similarity 100.0%; Pred. NO. 3.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 |||||  
 Db 8 CATAC 12

RESULT 7  
 BG929060  
 LOCUS HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BG929060  
 ACCESSION BG929060.1 GI:143233583  
 VERSION BG929060  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

IDENTIFICATION AND INITIAL CHARACTERIZATION OF 5000 EXPRESSED SEQUENCED TAGS (ESTs) EACH FROM ADULT HUMAN NORMAL AND OSTEOARTHRITIC CARTILAGE cDNA LIBRARIES  
 JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 UW2109

GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay\_kumar-1@gsk.com  
 Seq primer: T7.  
 Location/Qualifiers  
 1..17  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI; Directional"

## ORIGIN

Query Match 100.0%; Score 5; DB 12; Length 17;  
 Best Local Similarity 100.0%; Pred. NO. 3.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 |||||  
 Db 6 CATAC 10

RESULT 8  
 BG955683  
 LOCUS E012692-024-022-H17-SP6 MP1Z-ADIS-024-developing root Beta vulgaris cDNA clone 024-022-H17 5-PRIME, mRNA sequence.  
 DEFINITION BG955683  
 ACCESSION BG955683.1 GI:26125266  
 VERSION BG955683  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Herwig,A., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@piz-koeln.mpg.de  
 Insert Length: 17 Std Error: 0.00  
 Plate: 22 row: H column: 17  
 Seq primer: SP6; CATACGATTGAGTGACACTATAG.

FEATURES  
 source  
 1..17  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="taxon:161934"  
 /clone="024-022-H17"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-developing root"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:

```

b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
orientation:
SP6-Sall-CCACCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match      100.0%; Score 5; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db      |||||
3 CATAC 7

RESULT 9
C21103
LOCUS
DEFINITION HUMG0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
sequence.
C21103
VERSION C21103.1 GI:1622213
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Okubo, K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel.: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBEJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/notes="One or more human adult tissue"

ORIGIN
Query Match      100.0%; Score 5; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db      |||||
9 CATAC 13

RESULT 10
BM397954
LOCUS
DEFINITION 5009-0-39-G08.t.1 Chilcoat/turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397954
VERSION BM397954.1 GI:18198022
KEYWORDS EST.

b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
orientation:
SP6-Sall-CCACCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match      100.0%; Score 5; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db      |||||
3 CATAC 7

RESULT 9
C21103
LOCUS
DEFINITION HUMG0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
sequence.
C21103
VERSION C21103.1 GI:1622213
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Okubo, K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel.: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBEJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/notes="One or more human adult tissue"

ORIGIN
Query Match      100.0%; Score 5; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db      |||||
9 CATAC 13

RESULT 10
BM397954
LOCUS
DEFINITION 5009-0-39-G08.t.1 Chilcoat/turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397954
VERSION BM397954.1 GI:18198022
KEYWORDS EST.

```

```

Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomata; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 18)
AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL Contact: Turkewitz AP
COMMENT Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
Db      |||||
1 CATAC 5

RESULT 11
AA977115/c
LOCUS
DEFINITION Oq24c08.s1 NCI-CGAP GC4 Homo sapiens cDNA clone IMAGE:1587278 3',
similar to TR:Q69566 Q69566 ;, mRNA sequence.
ACCESSION AA977115
VERSION AA977115.1 GI:3154561
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Emmert-Buck, M.D., Ph.D.
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"

```

/db\_xref="taxon:9606"  
 /clone="IMAGE:1587278"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_GC4"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
 |||||  
 Db 13 CATAC 9

## RESULT 12

A1120725

LOCUS

DEFINITION ub72b11.r1 Soares\_mammary\_gland\_NMLMG Mus musculus cDNA clone IMAGE:1383261 5' similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:905729

Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 1.

Location/Qualifiers  
 1. .19  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1383261"  
 /sex="female (lactating)"  
 /tissue\_type="mammary gland"  
 /lab\_host="DH10B"

## FEATURES

source

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was

## ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CATAC 5  
 |||||  
 Db 7 CATAC 11

## RESULT 13

A1747751/c

LOCUS

DEFINITION

u121h05.x1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:2088249 3' similar to TR:P79101 P79101 CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR PROTEIN. ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:995933

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 1.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL"

/db\_xref="taxon:10090"

/clone="IMAGE:2088249"

/dev\_stage="embryo, 14 dpc"

/lab\_host="DH10B"

/clone\_lib="Sugano mouse embryo mewa"

/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTC); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTC, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments &lt;1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAAGCTGG and 3' end primer CGACCTGCAGCTCGAGCACA."

## ORIGIN

```

Query Match      100.0%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
    |||||
Db 17 CATAC 13

RESULT 14
BX551013/c
LOCUS
DEFINITION BX551013 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tsel16a12_glc, mRNA sequence.
ACCESSION BX551013
VERSION BX551013.1 GI:33374827
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
            Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 19)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kherhoun, A., Berriman, M.,
          Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
          Pathogen Sequencing Unit
          The Sanger Institute The Wellcome Trust Genome Campus
          Hinxton, Cambridge, CB10 1SA, UK
          Request for clones, please contact: Mike Lehane
          Prof. M.J.Lehane
          School of Biological Sciences,
          University of Wales,
          Bangor LL57 2UW
          All clones with suffix gic are reverse primer reads starting at 5'
          end of the cDNA all pic reads are from
          the 3' end.

FEATURES             Location/Qualifiers
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                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tsel16a12_glc"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /notes="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
    |||||
Db 12 CATAC 8

RESULT 15
C00646/c
LOCUS
DEFINITION HUMGS0008192 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
sequence.
ACCESSION C00646

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VERSION C00646.1 GI:1432876
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Okubo, K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo, K.
          Institute for Molecular and Cellular Biol
          Osaka University
          1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
          Tel: 06-877-5111 (ex.3315)
          Email: kousaku@imcb.osaka-u.ac.jp
          We are not submitting the same cDNA sequence redundantly to DBJ
          since 1993. For the abundance information of clones with this
          sequence in this library and as well as in other 3'-directed
          libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
          sequences of the clones represented by this GS sequences is also
          found there.

FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="adult"
                     /clone_lib="Human adult (K.Okubo)"
                     /note="One or more human adult tissue"

ORIGIN
Query Match      100.0%; Score 5; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5
    |||||
Db 18 CATAC 14

Search completed: August 11, 2004, 18:58:43
Job time : 607.215 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 17:57:26 ; Search time 15 Seconds  
(without alignments)  
184.984 Million cell updates/sec

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 carac 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:\*
- 1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*
  - 2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*
  - 3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*
  - 4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*
  - 5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq.\*
  - 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	5	100.0	5	3	Sequence 20, Appl
C 3	5	100.0	5	4	Sequence 4, Appl
C 4	5	100.0	5	4	Sequence 20, Appl
C 5	5	100.0	7	1	US-08-615-170-10
C 6	5	100.0	7	1	US-08-615-170-12
C 7	5	100.0	7	3	US-09-048-927-3
C 8	5	100.0	8	4	US-09-142-593-11
C 9	5	100.0	8	4	US-09-927-886-17
C 10	5	100.0	9	2	US-08-583-276-1
C 11	5	100.0	9	3	US-08-646-789A-8
C 12	5	100.0	9	3	US-08-646-789A-80
C 13	5	100.0	9	3	US-09-048-927-1
C 14	5	100.0	9	4	US-09-319-648-68
C 15	5	100.0	9	4	US-09-989-789-623
C 16	5	100.0	9	4	US-09-989-789-2220
C 17	5	100.0	9	4	US-09-989-789-2256
C 18	5	100.0	10	1	US-09-283-790-37
C 19	5	100.0	10	1	US-09-721-777-19
C 20	5	100.0	10	1	US-08-335-565A-27
C 21	5	100.0	10	1	US-08-250-951-1
C 22	5	100.0	10	1	US-08-232-233-1
C 23	5	100.0	10	1	US-08-222-177A-422
C 24	5	100.0	10	1	US-08-351-748-23
C 25	5	100.0	10	1	US-08-351-748-25
C 26	5	100.0	10	1	US-08-202-927-25
C 27	5	100.0	10	1	US-08-430-536A-23
C 28	5	100.0	10	1	US-08-430-536A-25

C 28	5	100.0	10	1	US-08-171-718-45	Sequence 45, Appl
C 29	5	100.0	10	2	US-08-703-601-1	Sequence 1, Appl
C 30	5	100.0	10	2	US-08-684-547-23	Sequence 23, Appl
C 31	5	100.0	10	2	US-08-684-547-25	Sequence 25, Appl
C 32	5	100.0	10	3	US-08-469-318-174	Sequence 174, App
C 33	5	100.0	10	3	US-08-468-609A-174	Sequence 174, App
C 34	5	100.0	10	3	US-08-478-087-45	Sequence 45, Appl
C 35	5	100.0	10	3	US-09-063-450-24	Sequence 24, Appl
C 36	5	100.0	10	3	US-09-063-450-33	Sequence 33, Appl
C 37	5	100.0	10	3	US-09-123-638-1	Sequence 1, Appl
C 38	5	100.0	10	3	US-08-646-695-30	Sequence 30, Appl
C 39	5	100.0	10	3	US-08-875-533-31	Sequence 31, Appl
C 40	5	100.0	10	4	US-08-446-872A-174	Sequence 174, App
C 41	5	100.0	10	4	US-09-724-753-1	Sequence 1, Appl
C 42	5	100.0	10	4	US-08-762-227A-174	Sequence 174, App
C 43	5	100.0	10	4	US-09-475-947A-23	Sequence 23, Appl
C 44	5	100.0	10	4	US-09-427-834A-34	Sequence 34, Appl
C 45	5	100.0	10	4	US-09-445-388A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-08-855-372B-20/c  
; Sequence 20, Application US/08855372B  
; Patent No. 6090549  
; GENERAL INFORMATION:  
; APPLICANT: Mirzabekov, Andrei D  
; APPLICANT: Parinov, Sergei V  
; APPLICANT: Barsky, Victor E  
; APPLICANT: Kirillov, Eugene V  
; APPLICANT: Dubiley, Svetlana A  
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagn  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHERSKOV & FLAYNIK  
; STREET: 20 N. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage  
; COMPUTER: PC  
; OPERATING SYSTEM: Microsoft Windows 98  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/855,372B  
; FILING DATE: 13-MAY-97  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/587,332  
; FILING DATE: 16-JAN-96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cherskov, Michael J.  
; REGISTRATION NUMBER: 33,664  
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 621-1330  
; TELEFAX: (312) 621-0088  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: No. 6090549 Applicable  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: yes  
US-08-855-372B-20

Query Match 100.0%; Score 5; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CATAC 5
Db      5 CATAC 1

RESULT 2
US-09-048-927-4/c
; Sequence 4, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-4

Query Match      100.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+08; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
Db      5 CATAC 1

RESULT 3
US-09-498-851-20/c
; Sequence 20, Application US/09498851
; Patent No. 6440671
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous
; TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,851
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/855,372
; FILING DATE: 13-MAY-97
; APPLICATION NUMBER: U.S. 08/587,332

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; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANI-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6440671 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: yes
; US-09-498-851-20

Query Match      100.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+08; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
Db      5 CATAC 1

RESULT 4
US-08-615-170-10
; Sequence 10, Application US/08615170
; Patent No. 5776776
; GENERAL INFORMATION:
; APPLICANT: ORDAHL, Charles P.
; APPLICANT: AZAKIE, Anthony
; APPLICANT: MAR, Janet H.
; APPLICANT: FARRANCE, Iain K.G.
; APPLICANT: HALL, Deborah E.
; APPLICANT: STEWART, Alexandre F.R.
; APPLICANT: LARKIN, Sarah B.
; TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,170
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01526
; FILING DATE: 06-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/191,493
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 2307U-053120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:

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SEQUENCE CHARACTERISTICS:  
LENGTH: 7 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:

NAME/KEY: misc feature

LOCATION: 1..7

OTHER INFORMATION: /standard\_name= "Sph-II binding

OTHER INFORMATION: site in SV40"

US-08-615-170-10

Query Match 100.0%; Score 5; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred.No. 7.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 1 CATAC 5

#### RESULT 5

US-08-615-170-12

Sequence 12, Application US/08615170

Patent No. 5776776

GENERAL INFORMATION:

APPLICANT: ORDAHL, Charles P.

APPLICANT: AZAKIE, Anthony

APPLICANT: MAR, Janet H.

APPLICANT: FARRANCE, Iain K.G.

APPLICANT: HALL, Deborah E.

APPLICANT: STEWART, Alexandre F.R.

APPLICANT: LARKIN, Sarah B.

TITLE OF INVENTION: DREF-1 ISOFORMS AND USES THEREOF

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: Stewart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/615,170

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01526

FILING DATE: 06-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/191,493

FILING DATE: 04-FEB-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 2307U-053120

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..7

OTHER INFORMATION: /standard\_name= "Rat beta-Myosin

OTHER INFORMATION: Heavy Chain M-CAT binding element"

US-08-615-170-12

Query Match

Best Local Similarity 100.0%; Score 5; DB 1; Length 7;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 1 CATAC 5

#### RESULT 6

US-09-048-927-3/c

Sequence 3, Application US/09048927

Patent No. 6147056

GENERAL INFORMATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Vaar, Mina

APPLICANT: Ellser, Mark

TITLE OF INVENTION: Use of Locally Applied DNA Fragments

FILE REFERENCE: BU94-68A2

CURRENT APPLICATION NUMBER: US/09/048,927

CURRENT FILING DATE: 1998-03-26

EARLIER APPLICATION NUMBER: 08/952,697

EARLIER FILING DATE: 1996-06-03

EARLIER APPLICATION NUMBER: 08/467,012

EARLIER FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 7

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: DNA Fragment

US-09-048-927-3

Query Match

Best Local Similarity 100.0%; Score 5; DB 3; Length 7;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 6 CATAC 2

#### RESULT 7

US-09-142-593-11

Sequence 11, Application US/09142593

Patent No. 6489458

GENERAL INFORMATION:

APPLICANT: HACKETT ET AL.

TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE

TITLE OF INVENTION: INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MINNESOTA

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/142,593  
 ; FILING DATE: 10-SEP-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/040,664  
 ; FILING DATE: 11-MAR-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/053,868  
 ; FILING DATE: 28-JUL-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/065,303  
 ; FILING DATE: 13-NOV-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US98/04687  
 ; FILING DATE: 11-MAR-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SANDBERG, VICTORIA A.  
 ; REGISTRATION NUMBER: 41,287  
 ; REFERENCE/DOCKET NUMBER: 110.00450101  
 ; TELEPHONE: 612-305-1226  
 ; TELEFAX: 612-305-1228  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-09-142-593-11

Query Match 100.0%; Score 5; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 DB 2 CATAC 6

RESULT 8  
 ; Sequence 17, Application US/09927886  
 ; Patent No. 6613752  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kay, Mark A.  
 ; TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a  
 ; TITLE OF INVENTION: Sleeping Beauty Transposon System  
 ; FILE REFERENCE: STAN-160CIP  
 ; CURRENT APPLICATION NUMBER: US/09/927,886  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: 60/162,279  
 ; PRIOR FILING DATE: 1999-10-28  
 ; PRIOR APPLICATION NUMBER: 09/440,301  
 ; PRIOR FILING DATE: 1999-11-17  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 17  
 ; LENGTH: 8  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: transposon repeat sequence  
 ; US-09-927-886-17

Query Match 100.0%; Score 5; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 DB 2 CATAC 6

Db 2 CATAC 6

RESULT 9  
 ; US-08-583-276-1/c  
 ; Sequence 1, Application US/08583276  
 ; Patent No. 5837536  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McDonagh, Kevin T.  
 ; APPLICANT: Nienhuis, Arthur  
 ; APPLICANT: Tolstoshev, Paul  
 ; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN  
 ; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED  
 ; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
 ; ADDRESSEE: Cecchi & Stewart  
 ; STREET: 6 Becker Farm Road  
 ; CITY: Roseland  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07068

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch diskette  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: DM4 V2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/583,276  
 ; FILING DATE: 05-JAN-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/332,444  
 ; FILING DATE: 31-OCT-1994  
 ; APPLICATION NUMBER: 07/887,712  
 ; FILING DATE: 22-MAY-1992  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 bases  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: singular  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE:  
 ; DESCRIPTION: Genomic DNA  
 ; US-08-583-276-1

Query Match 100.0%; Score 5; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 DB 8 CATAC 4

RESULT 10  
 ; US-08-646-789A-8/c  
 ; Sequence 8, Application US/08646789A  
 ; Patent No. 6022863  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Peyman, John A.  
 ; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 101  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,789A  
FILING DATE: May 21, 1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6523-006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-646-789A-8

Query Match 100.0%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.8e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 5 CATAC 1

RESULT 11  
US-08-646-789A-80/c  
Sequence 80, Application US/08646789A  
Patent No. 6022863  
GENERAL INFORMATION:  
APPLICANT: Peyman, John A.  
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,789A  
FILING DATE: May 21, 1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6523-006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-646-789A-80

Query Match 100.0%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.8e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 5 CATAC 1

RESULT 12  
US-09-048-927-1/c  
Sequence 1, Application US/09048927  
Patent No. 6147056  
GENERAL INFORMATION:  
APPLICANT: Gilchrist, Barbara A.  
APPLICANT: Yaar, Mina  
APPLICANT: Eller, Mark  
TITLE OF INVENTION: Use of Locally Applied DNA Fragments  
FILE REFERENCE: BU94-68A2  
CURRENT APPLICATION NUMBER: US/09/048,927  
CURRENT FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: 08/952,697  
EARLIER FILING DATE: 1996-06-03  
EARLIER APPLICATION NUMBER: 08/467,012  
EARLIER FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DNA Fragment  
US-09-048-927-1

Query Match 100.0%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.8e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 7 CATAC 3

RESULT 13  
US-09-319-648-68  
Sequence 68, Application US/09319648  
Patent No. 6451530  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Mary  
TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin  
Formation for Detection of Nucleic Acid Hybridization  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/319,648  
FILING DATE: 30-Jul-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/032,844  
FILING DATE: 13-DEC-1996

```
;
; APPLICATION NUMBER: WO PCT/US97/22448
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fang, Carol
; REGISTRATION NUMBER: 48,631
; REFERENCE/DOCKET NUMBER: 015280-288100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-319-648-68

Query Match          100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
Db      3 CATAC 7

RESULT 14
US-09-989-789-623
; Sequence 623, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 623
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-623

Query Match          100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
Db      2 CATAC 6

RESULT 15
US-09-989-789-2220/c
; Sequence 2220, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2220

; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2220

Query Match          100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
Db      8 CATAC 4

Search completed: August 11, 2004, 19:33:23
Job time : 17 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 19:00:04 ; Search time 72.0968 Seconds  
(without alignments)  
340.279 Million cell updates/sec

Title: US-09-540-843-6  
Perfect score: 5  
Sequence: 1 catac 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 2263564

Minimum DB seq length: 0  
Maximum DB seq length: 200

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA: \*

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3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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13:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
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19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	5	100.0	5	15	US-10-122-630-6
C 3	5	100.0	5	15	US-10-122-633-4
C 4	5	100.0	5	15	US-10-122-633-6
C 5	5	100.0	7	13	US-10-027-632-178029
C 6	5	100.0	7	13	US-10-027-632-178043
C 7	5	100.0	7	15	US-10-122-630-3
C 8	5	100.0	7	15	US-10-122-630-7
C 9	5	100.0	7	15	US-10-122-633-3
C 10	5	100.0	7	15	US-10-122-633-7
C 11	5	100.0	7	16	US-10-027-632-178029
C 12	5	100.0	7	16	US-10-027-632-178043
C 13	5	100.0	8	9	US-09-142-593-11
C 14	5	100.0	8	9	US-09-927-886-17

15	5	100.0	8	9	US-09-861-014-6
C 16	5	100.0	8	13	US-10-314-578-1138
C 17	5	100.0	8	15	US-10-263-159-11
C 18	5	100.0	8	15	US-10-128-560-224
C 19	5	100.0	8	15	US-10-191-698-11
C 20	5	100.0	8	17	US-10-332-914-5
C 21	5	100.0	8	17	US-10-608-516-17
C 22	5	100.0	9	9	US-09-989-789-623
C 23	5	100.0	9	9	US-09-989-789-2220
C 24	5	100.0	9	9	US-09-989-789-2256
C 25	5	100.0	9	10	US-09-990-186-623
C 26	5	100.0	9	10	US-09-990-186-2220
C 27	5	100.0	9	10	US-09-989-994-623
C 28	5	100.0	9	10	US-09-989-994-2220
C 29	5	100.0	9	10	US-09-989-994-2256
C 30	5	100.0	9	15	US-10-122-630-1
C 31	5	100.0	9	15	US-10-122-633-1
C 32	5	100.0	9	15	US-10-096-596-32
C 33	5	100.0	9	16	US-10-378-558A-13
C 34	5	100.0	9	17	US-10-427-629-3
C 35	5	100.0	10	8	US-08-935-377-16
C 36	5	100.0	10	9	US-09-822-250-16
C 37	5	100.0	10	9	US-09-398-399-31
C 38	5	100.0	10	9	US-09-989-789-622
C 39	5	100.0	10	9	US-09-989-789-636
C 40	5	100.0	10	9	US-09-989-789-1338
C 41	5	100.0	10	9	US-09-989-789-1341
C 42	5	100.0	10	9	US-09-989-789-1342
C 43	5	100.0	10	9	US-09-989-789-1343
C 44	5	100.0	10	9	US-09-899-381-31
C 45	5	100.0	10	9	US-09-899-381-31

## ALIGNMENTS

RESULT 1  
US-10-122-630-4/c  
; Sequence 4, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Vaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-4

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.4e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 6, Appli  
Sequence 1138, Ap  
Sequence 11, Appl  
Sequence 224, App  
Sequence 11, Appl  
Sequence 5, Appli  
Sequence 17, Appl  
Sequence 623, App  
Sequence 2220, Ap  
Sequence 2256, Ap  
Sequence 623, App  
Sequence 2220, Ap  
Sequence 2256, Ap  
Sequence 623, App  
Sequence 2220, Ap  
Sequence 2256, Ap  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 32, Appl  
Sequence 13, Appl  
Sequence 3, Appli  
Sequence 16, Appl  
Sequence 31, Appl  
Sequence 622, App  
Sequence 636, App  
Sequence 1338, Ap  
Sequence 1341, Ap  
Sequence 1342, Ap  
Sequence 1343, Ap  
Sequence 31, Appli

QY 1 CATAC 5  
|||||  
Db 5 CATAC 1

## RESULT 2

US-10-122-630-6  
; Sequence 6, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-6

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.4e+08; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATAC 5  
|||||  
Db 1 CATAC 5

## RESULT 3

US-10-122-633-4/c  
; Sequence 4, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-4

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.4e+08; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATAC 5  
|||||  
Db 5 CATAC 1

## RESULT 4

US-10-122-633-6  
; Sequence 6, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-6

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.4e+08; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATAC 5  
|||||  
Db 1 CATAC 5

## RESULT 5

US-10-027-632-178029  
; Sequence 178029, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 178029
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178029

Query Match      100.0%; Score 5; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
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Db      1 CATAC 5

RESULT 6
US-10-027-632-178043
; Sequence 178043, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178043
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178043

Query Match      100.0%; Score 5; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
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Db      1 CATAC 5

RESULT 7
US-10-122-630-3/c
; Sequence 3, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; OLIGONUCLEOTIDES
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; GENERAL INFORMATION:
; RESULT 9
US-10-122-633-3/c
; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
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; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-3

Query Match      100.0%; Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
      |||||
Db      6 CATAC 2

RESULT 8
US-10-122-630-7/c
; Sequence 7, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; OLIGONUCLEOTIDES
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-7

Query Match      100.0%; Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
      |||||
Db      6 CATAC 2

RESULT 9
US-10-122-633-3/c
; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
```

; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-3

Query Match 100.0%; Score 5; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
Db 6 CATAC 2

RESULT 10  
US-10-122-633-7/c  
; Sequence 7, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 7  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-7

Query Match 100.0%; Score 5; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
Db 6 CATAC 2

RESULT 11  
US-10-027-632-178029  
; Sequence 178029, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 178029  
; LENGTH: 7  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-178029

Query Match 100.0%; Score 5; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
Db 1 CATAC 5

RESULT 12  
US-10-027-632-178043  
; Sequence 178043, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 178043  
; LENGTH: 7  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-178043

Query Match 100.0%; Score 5; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 1 CATAC 5

RESULT 13  
US-09-142-593-11  
; Sequence 11, Application US/09142593  
; Patent No. US20020016975A1  
; GENERAL INFORMATION:  
; APPLICANT: HACKETT ET AL.  
; TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE  
; INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.  
; STREET: 119 NORTH FOURTH STREET, SUITE 203  
; CITY: MINNEAPOLIS  
; STATE: MINNESOTA  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/142,593  
; FILING DATE: 10-SEP-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/040,664  
; FILING DATE: 11-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/053,868  
; FILING DATE: 28-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/065,303  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/04687  
; FILING DATE: 11-MAR-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDBERG, VICTORIA A.  
; REGISTRATION NUMBER: 41,287  
; REFERENCE/DOCKET NUMBER: 110.00450101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1226  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-142-593-11

Query Match 100.0%; Score 5; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.9e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 2 CATAC 6

RESULT 14  
US-09-927-886-17  
; Sequence 17, Application US/09927886  
; Patent No. US20020103152A1  
; GENERAL INFORMATION:  
; APPLICANT: Kay, Mark A.

; APPLICANT: Yant, Stephen  
; TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a  
; FILE REFERENCE: STAN-160CIP  
; CURRENT APPLICATION NUMBER: US/09/927,886  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/162,279  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 09/440,301  
; PRIOR FILING DATE: 1999-11-17  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: transposon repeat sequence  
US-09-927-886-17

Query Match 100.0%; Score 5; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.9e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 2 CATAC 6

RESULT 15  
US-09-861-014-6  
; Sequence 6, Application US/09861014  
; Patent No. US20020115216A1  
; GENERAL INFORMATION:  
; APPLICANT: Steer, Clifford  
; APPLICANT: Kren, Betsy  
; APPLICANT: Linehan-Stieers, Cheryle  
; APPLICANT: McIvor, R.  
; APPLICANT: Hackett, Perry  
; TITLE OF INVENTION: Composition for Delivery of Compounds to Cells  
; FILE REFERENCE: 110.01330101  
; CURRENT APPLICATION NUMBER: US/09/861,014  
; CURRENT FILING DATE: 2001-05-19  
; PRIOR APPLICATION NUMBER: US 60/206,002  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/285,121  
; PRIOR FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Direct repeat sequence  
US-09-861-014-6

Query Match 100.0%; Score 5; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.9e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 2 CATAC 6

Search completed: August 11, 2004, 21:11:06  
Job time : 73.4301 secs

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